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Result
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                    Score
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length: 2000000000
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Match
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                                                                                                          Issued Patents AA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                    Length DB
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896
896
  GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-323-873A-2
US-09-134-001C-5278
US-09-247-373B-54
US-08-403-866-2
US-08-651-999A-7
US-08-651-999A-7
US-08-061-376-5
US-08-468-709B-16
US-08-252-995D-2
US-08-834-108-2
US-08-834-108-6
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US-08-834-108-8
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US-08-834-108-8
US-08-95D-4
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Sequence 7, Appli
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Sequence
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    Sequence
              537,
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	Sequence	US-08-484-635-148	PCT-US92-06840-2	US-09-650-855-7	US-09-651-656-7	US-08-980-357-29	US-08-286-819A-29	US-09-004-838-108	US-07-853-913-2	US-09-149-934-4	US-09-249-003-2	US-08-345-212-2	US-08-484-494-2	US-08-484-493-2	US-09-134-001C-5673	US-09-052-778-13	US-09-134-001C-3418	US-09-359-161-3	

ALIGNMENTS

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APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Appulicant
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
Sequence 5278, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-323-873A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-323-873A-2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Daniel E. Afar APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                  14 WKMKPRRNLEEDDYL 28
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ilarity 100.0%;
Conservative 0
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Pred. No. 9.5e-07;
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FILE REPERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 54
LENGTH: 221
TYPE: PRT
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5278
LENGTH: 256
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Patent No. 5643779
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Best Local (
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APPLICANT: O'KEEFE, DANIEL
ATTLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 207-
                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 APPLICANT: Ehrlich, Stanislav
APPLICANT: Godon, Jean-Jacques
APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: synthase from Lactococcus and its applications
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION:
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Local Similarity 64.3%;
les 9; Conservarium
                                                                                                                             APPLICATION NUMBER: FILING DATE:
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Local Similarity 44.4%;
les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                 US/08/403,866
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                    20747/30
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Pred. No. 27;
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Pred. No. 1
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1 WKMKPRRNLEEDD 13

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; INDIVIDUAL ISOLATE: LEUB
US-08-403-866-2
                                                             ; DESCRIPTION:
; HYPOTHETICAL:
US-08-651-999A-7
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                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/651,999A
FILING DATE: MAY 23, 1996
ATTONNEY/AGENT INFORMATION:
NAME: BLIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 267-5995
TELEFAX: (212) 26-0854 or 286-0082
INFORMATION FOR SEQ ID NO: 7:
INFORMATION FOR SEQ ID NO: 7:
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Query Match
Best Local S
Matches 6
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Patent No. 6
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (716) 263-1487
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 968 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: pi
                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stefan Somlo and Toshio Mochizuki
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 KLSPIRNVENVDFL 127
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YORK
Local Similarity 46.
                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC COMPATIBLE
                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMSTER, ROTHSTEIN & EBENSTEIN
                                                                             : peptide
NO
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                44.2%;
46.2%;
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Pred. No.
Score 38; DB 3;
Pred. No. 2.9e+02;
2; Mismatches 5
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94;
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                                Length 968;
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    Indels
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293 WKMQPSNQTEADN 305

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US-09-385-752-7
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GENERAL INFORMATION:
APPLICANT: Stefan
                                                                                                                                                                  Sequence 5, Application US/08061376 Patent No. 6175000
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/385,752
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/651,999
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGGSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/395
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                    GENERAL INFORMATION:
         APPLICANT: Evans, Glen A.

APPLICANT: Djabail, Malek
APPLICANT: Selleri, Licia
APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYCYSTIC KIDNE: TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   293 WKMQPSNQTEADN 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stefan Somlo and Toshio Mochizuki
JENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC COMPATIBLE SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                          Db ;
2.9e+02;
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RESULT 8
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Best Local Similarity 60.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08468709B Patent No. 5654137
         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,709B
FILING DATE: 06/06/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 2115-00676DVF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Astrom, Anders
APPLICANT: Voorhees, John
APPLICANT: Pattersson, Ulrika
APPLICANT: Tavakkol, Amir
TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 PRRFIEDEDY 433
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STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 13-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 48303
                                                                                                                                                                                                                                                                                                                                      CITY: Bloomfield Hills
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                 Michigan United States of America
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PO Box 828
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(810) 641-1600
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 Mismatches

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Pred. No. 1.4e+03;
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RESULT 10
US-08-969-106-4
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; Sequence 16, Application US/08241664B
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                                                                                                                                                                                                    ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-241-6648-16
                                                                                                                                                                                                                    TELEFAX: (b1.
TELEX: 287637
TELEX: 287637
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TVDE: amino acids
TVDE: amino acids
TVDE: amino acids
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                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,664B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGENCE/DOCKET NUMBER: 2115-00676COD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.0%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (810) 641-027
TELEX: 287637
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Voorhees, John J.
APPLICANT: Astrom, Anders
APPLICANT: Pattersoon, Ulrika
APPLICANT: Tavakkol, Amir
TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: M
                                                                                                                              / Match 43.0%;
Local Similarity 54.5%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48303
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                                                                                                  1 WKMKPRRNLEE 11
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                                                                    WKMRSSENFEE 17
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/: United States of America
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PO Box 828
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Pred. No.
                                                                                                                                                   Score 37; DB 2;
Pred. No. 7.9;
                                                                                                                                     Mismatches
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                                                                                                                                                                   Length 25;
                                                                                                                                   4; Indels
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; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-969-106-4
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US-08-252-995D-2
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Patent No. 5986055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.0%; Score 37; DB 2; Best Local Similarity 50.0%; Pred. No. 1.3e+02 Matches 6; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
COUNTRY: Canada
ZIP: M5H 3Y2
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OP INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,
FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 KKRKGYEDDDYV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                           CITY: Toronto
                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-790-900
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 79
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                                                                                                                                                                    Ontario
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SYSTEM: DOS
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US-08-834-108-2
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                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834.104
FILING DATE:
CLASSTEYTT:
                              Best Local Similarity 54.1 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5976893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                             Query Match
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TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                       TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BERBSKIN & PARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 KPRRSLDENQH 416
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Local Similarity 54.5%;
nes 6; Conservative
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                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,971 REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
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4 KPRRNLEEDDY 14
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                                                                                                                                                          416 amino acids
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                                                                                                                                                                                                                            (416) 364-7311
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                                             43.0%;
54.5%;
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Pred. No. 1.7e+02
                                             Score 37;
Pred. No.
                                             DB 2; I
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US-08-252-995D-6
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                                                                                                                                                                                                                                                                                                     RESULT 14
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
PILING DATE: 02-UN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    Sequence 6, Application US/08834108 Patent No. 5976893
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 464 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dennis
                                                                                                                                 APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL 9
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: **
STREET: Toronto
Ontario
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                                                                    STREET: 40 Kin
CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                         406 KPRRSLDENOH 416
                                  STATE: Ontario COUNTRY: Canada ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                    ADDRESSEE:
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                                                                                                 40 King Street West
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                                                                                                                    BERESKIN & PARR
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54.5%;
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Pred. No. 1
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1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.0%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                  APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE:
CLASSYPTATE
CLASSYPTATE
OPERATOR NUMBER; US/08/874
                                                                                                                                                                                                                         ZIP: 941114187

COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RINE, Jasper
APPLICANT: MCNALLY, Francis J
APPLICANT: LAURENSON, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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406 KPRRSLDENQH 416
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                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEB: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KPRRNLEEDDY 14
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                       (415) 494-8771
10 277299
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KOBAYASHI, Ryuji
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Pred. No. 1.9e+02;
4; Mismatches 1
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Query Match
Best Local Similarity
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Search completed: March 26, 2003, 16:51:37 Job time: 11.593 secs
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                                                                                                                                                US-08-484-105-24 ·
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                  52 KPEYDLEEDD 61
                                                                        4 KPRRNLEEDD 13
                                                                                                 Conservative
                                                                                                             43.0%;
70.0%;
                                                                                                  1;
                                                                                                             Score 37;
Pred. No.
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Title:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
A Geneseq 101002:*

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3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match Length DB	ength	BO	ID	Description
1	86	- 4	15	21	AAY58201	Human STRAP-1 pept
N	86	100.0	15	22	AAE02784	Immunogenic peptid
w	86	100.0	66	20	AAY12305	Human 5' EST secre
4.	86	100.0	109	20	AAY12304	Human 5' EST secre
u	86	100.0	339	21	AAY58194	Human STRAP-1 prot
σ,	86	100.0	339	22	AAU69927	Human prostate cDN
7	86	100.0	339	22	AAM78845	Human protein SEQ
80	98	100.0	339	22	AAM01282	P789P amino acid s
9	86	100.0	339	23	ABG61813	Prostate cancer-as
10	86	100.0	339	23	ABB95387	Human P789P protei

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98US 98US 98US	99W0			nsmembra domain; r; bladd ; tumour ral; ant itoring; g; recom	peptide	irst													-	 .												
-0087 -0091 INC.	99WO-US12157			ransmembrane antige e domain; type IIIa cer; bladder cancer er; tumour antigen; moral; anticancer v onitoring; suscepti ing; recombinant pr	de 1,	entr		pepti			257 258	236	224	223	205 221	197	738	327 327	271	166	1417	996	959	165	164	156	2040	421 1106	72	9 r 19 r	375	374
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				membra; colon immuni accine; bility; otein.	corresponding			15 AA.	ALIGNMENTS		ABP30273 ABP25968	ABP29691	AAG39745	AAB62225	AAG38584 AAB07850	AAW98006	ABB65092	AAM40194 ABB06781	AAG30005	AAG30007	ABB63329	AAU75900 AAU07892	AAU07874	AAG67877	AAB35757	ABF40433 ABG04393	ABB04597	ABG25522 ABG25523	ABG25517	AAY11840	AAE02780	AAM79829
				e prostate; STRAP-1; prostate; ne protein; expression; cancer cancer; pancreatic cancer; sation; immune response; antibody; detection; diagnosi therapeutic inhibitor;	to STRAP-1 residues 14-28.					,	Streptococcus Streptococcus	Streptococcus	Arabidopsis t Arabidopsis t	Glycine max g	Arabidopsis t Amino acid se	Human interle	Drosophila me Gene 41 Human	Human polypep	Arabidopsis ti	Arabidopsis thalia	Drosophila me	Human Testis Polypeptide s	Polypeptide s	Equine infectious	EIAV rev gene	Novel human diagno	. =	Novel human d Novel human d	1 human	Human 5' EST : Kidnev injurv	Bix tr	Human protein
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RESULT 2
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AC AAE0
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                                                                                                                                                                                                                                                                                                                                                                               Ct the prostate A-28 of SIRAP-1 (SETEPHILIE TRAINMENDIATE anti-Spen of the prostate, AAVSS194). This peptide was used to raise

C polyclonal anti-STRAP-1 N-terminus antibodies in sheep. The

CC antibodies were used to probe Western blots of cell lysates from

CC prostate and mon-prostate cancer cell lines, and in immunohistochemical

CC analysis of STRAP-1 expression. STRAP-1 is the prototype

CC exhibit a high degree of structural conservation, but which show

CC no significant structural homology to known human proteins. The STRAP-1

CC gene has been localised to chromosome 7922. STRAP-1 is thought to be a

CC type IIIa membrane protein and is expressed predominantly in prostate

CC cells in normal human tissues. Structurally, STRAP-1 is a 339 amino

CC acid protein characterised by six transmembrane domains and

CC intracellular N- and C-termini, suggesting that it folds in a

CC syrap-1 manar into three extracellular and two intracellular loops.

CC syrap-1 manar and protein expression is maintained at high levels and

CC syrap-1 mana and protein expression is maintained at high levels and

CC syrap-1 mana and protein expression is maintained at high levels and

CC syrap-1 mana and protein expression is maintained at high levels and

CC syrap-1 mana and protein expression is maintained at high levels and

CC syrap-1 mana and protein expression is maintained at high levels and

CC syrap-2 are cell-surface tumour antigens. Immunisation with a STRAP

CC specific binding agents, to produce antigens. Immunisation with a STRAP-1 and

CC syrap-2 are cell-surface tumour antigens. Immunisation with a STRAP

CC specific antibodies. The antibodies may be used for detection, prognosis,

CC and monitoring of cancers (or susceptibility to cancer), as therapeutic

CC modulation/inhibition of STRAP expression. Since high levels of STRAP

CC specific and prognostic reagents, for identifying STRAP-expressing

CC inhibitors of syrap expression. Since high levels of STRAP

CC specific and prognostic reagents for they are easil
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3C; Page 41; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly for prostatic cancer
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(RAIT/)
(SAFF/)
                 Immunogenic
                                                       06-AUG-2001
                                                                                            AAE02784;
                                                                                                                               AAE02784 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                 1 WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins useful as diagnostic markers and therapeutic targets
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RAITANO A B.
SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                                                                               15 AA;
               peptide
                                                                                                                                                                                                                                                                                                        Conservative
                                                       (first entry)
               #1 of human STEAP-1
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100.0%; Pr
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                        4.6e-08;
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                                                                                                                                                                                                                                                                                                                                          Length 15;
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comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, and is sequence to the cancer cells and the encoded single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly. The present sequence is an immunogenic peptide of STEAP-1. STEAP-1 gene is located on chromosome 7p22.3. This peptide is used to immunise sheep for the generation of sheep polyclonal antibodies towards the amino-terminus of anti-STEAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; ovarian; lung; serpentine transmembrane antigen; immunogen.
                                                                                                                                                                                                                                                                                       The present invention relates to human six transmembrane epithelial antigen of the prostate (STEAP) protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP gene is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2000; 2000WO-US33040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3C; Page 77; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New STEAP (six transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-367804/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, expressed in human
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  15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelial antigen of the prostate) cancers, useful for detecting and treating
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                   Matches
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Best Local (
1 WKMKPRRNLEEDDYL 15
                   15;
                           Similarity
                   Conservative
                          100.0%;
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Pred. No.
                    Mismatches
                           4.6e-08;
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RESULT 4
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                                                        Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haematory activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human secreted proteins, and encode the proteins given in AAY12261 AAY12514, respectively. The proteins given represent the signal per and an N-terminal fragment of a secreted protein. The nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Page 677-678; 824pp; English.
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                                                                                                                                                           Human 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding human secreted proteins - obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1999
                                              thrombolytic;
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nes 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 libraries prepared from e.g. liver, ovary, brain, prostate, ey, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                      WKMKPRRNLEEDDYL 15
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                                                                                                                                                        secreted protein SEQ ID NO:335.
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                                            anti-inflammatory; tumour inhibition
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Pred. No.
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Homo

sapiens

/note= "Intracellular region

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Best Local Similarity
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                               Key
Region
                                                                                                                                                                                                               Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; colon cancer; colon cancer; immunistation; immune response; cellular; humoral; antigen; immunistation; immune response; prognosis; monitoring; susceptibility; therapeutic inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12261 to AAY12514, respectively. The proteins given represent the signal peptia and an N-terminal fragment of a secreted protein. The nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Human STRAP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY58194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A,
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                                                                                                                            Homo sapiens.
                                                                                                                                                                                     grug
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                                                                                                                                                                                  targetting; recombinant
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Pred. No. 3.8e-07;
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Domain

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This sequence represents a novel human protein, STRAP-1 (serpentine cransmembrane antigen of the prostate). STRAP-1 is the prototype caxhibit a high degree of structural conservation, but which show come has been localised to chromosome 7p2. STRAP-1 is thought to be a cype life and protein and is expressed predominantly in prostate call protein characterised by six transmembrane domains and cointracellular N- and C-termini, suggesting that it folds in a cyperested in cartain other cancer. STRAP-1 hat high levels and chromosome 7p2. STRAP-1 is a 39 amino capture manner into three extracellular and two intracellular loops. STRAP-1 mRNA and crotein expression is maintained at high levels and chromosome strapes of prostate cancer. STRAP-1 mRNA and/or protein is grap-junction protein cancer. The function of the STRAP protein is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or grap-junction proteins (from immunorial immunor ersponses against STRAP-1 and STRAP-2 are cellular and humoral immunor responses against content induces cellular and humoral immunor responses against specific-binding agents, to produce anticancer vaccines and to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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DB; AAZ49395, AAZ49396.
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HUBERT R S.
LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig
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98US-0091183.
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12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0636783.
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0651279.
02-OCT-2000; 2000US-0679426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2002
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N-PSDB; AAS64160.
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09-MAY-2000; 2000US-0568100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
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                                                                                                                                                                                                                  human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon DC,
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                                                                                                                                                                                                                                                                                                                                                                               , Mitcham JL, Harlocker er MW, Stolk JA, Day CH, Skeiky YAW, Hepler WT, I
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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                                                                                                                                                                                                                                                                                                                                                                                                              Kalos MD;
Carter D;
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence

the presence of

549;

579pp; English.

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RESULT 7
AAM78845
ID AAM78845
AAM7845
AAM78845
AAM78645
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Best Local S
Matches 15
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-063936.
15-SEP-2000; 2000US-0639325.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
The invention relates to polymucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM78322-AAM60302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy. Vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476283/51.
N-PSDB; AAK51978.
                                                                                                                                                                                                                                                                                                                                                                                                                             Xue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                                              Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1507.
                                                                                                                                                                                                              3800-3801; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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F, C
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Wang
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cc and can be used in vaccine production and (II) have cytostatic activity,

cc antibodies to (II), fusion proteins comprising (II), and isolated

cc rells prepared using (I) or (II) are used treat cancer in a patient.

cc (I) and the antibodies are also used in the detection of cancer in a

cc patient. The cancer that is diagnosed or treated is particularly

cc prostate cancer. (I) and (II) can be used in vaccines. The antibodies or

cc (I) and (II) can also be used to rested is particularly

cc methods for prostate cancer. They can indicate the level of metastasis

as well as the prostate volume. AAH93357 to AAH01318 represent polymuclectide and anino acid sequences used in the

cc exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                        Claim 2; Page 510-512; 543pp; English.
                                                                                                                                                                                                                              New polynucleotide encoding diagnosing, monitoring and to for use in vaccines -
                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200151633-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P789P amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000; 2000US-0483672.
                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
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MD, Fanger GR, Day
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                                                                                                                                                                                                                                                                                                      Meagher MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; prostate-specific; diagnosis; vaccine;
therapy; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                          oding a prostate-specific protein, and treating prostate cancer in a
                                                                                                                                                                                                                                                                                                                 HH.
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Pred. No.
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Retter MW, Stolk
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from
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olk JA, Skeiky
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the sequenc
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sequence listing
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Sequence

DB 22;

Length 339;

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RESULT 9
ABG61813
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                               The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer as well as for identifying modulators of prostate cancer as gents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
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Best Local Similarity
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                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC. by determining if prostate cancer-associated genes are expressed in a prostate tissue
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16-MAR-2001;
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08-DEC-2000;
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer; prostate tumour tissue; human; mammal; cytostatic
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                          ABG61800-ABG61944 represent prostate cancer-associated
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                                                                                                                                                                                                                                           Page 312; 436pp; English
                                                                                                                                                                                                                                                                                                                                                                       Mack DH,
 339
                                                                                                                                                                                                                                                                                                                                                                                                BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-276888P.
; 2001US-281922P.
; 2001US-286214P.
; 2001US-0847046.
; 2001US-288589P.
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2000US-0733742.
2001US-263957P.
2001US-276791P.
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                                                                                                                                                                                                                                                                                                                                                                       Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein #14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         P;
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                          proteins
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Best Local S
Matches 15
                                                                                                                                                                                        12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                                      25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
                                                                                                                         (XUJJ/)
                                                                                                                                                                                                              27-MAR-2000;
09-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       Human P789P protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB95387;
Xu J, Dillon DC, Mit Fanger GR, Retter MW,
                                                  (CART/
                                                                (RETT/
(STOL/
(DAYC/
(VEDV/
                                                                                            (KALO/)
                                                                                                          (HARL/)
                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                                                                                           13-JUL-1999;
12-NOV-1999;
                                                                                                                                                                                                                                                                                                                        12-JAN-2001; 2001US-0759143
                                                                                                                                                                                                                                                                                                                                       21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                     US2002022248-A1
                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB95387 standard;
                                                                                                                                                      10-OCT-2000;
                      (HEND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                       cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                            LISX.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                    JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                 MITCHAM J L.
HARLOCKER S L.
                                                                                                                                         검
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                     HENDERSON R A.
                                                          CARTER D.
                                                                                                                                DILLON
                                                                                                                                         <u>-</u>
                                                                                                                                                            ; 2000US-0651236.
; 2000US-0657279.
; 2000US-0679426.
                                                                                                                                                                                2000US-0568100.
2000US-0570737.
2000US-0593793.
2000US-0605783.
2000US-0636215.
                                                                                                                                                                                                                    99US-0288946.
99US-0352616.
99US-0439313.
99US-0443685.
2000US-04436672.
2000US-0536857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                       2000US-0685166
                                                                                                                                                                                                                                                              98US-0030607.
98US-0115453.
98US-0159812.
99US-0232149.
                                                                                                                                U
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 339
Mitcham JL, Harlocker SL, Jiang Y, MW, Stolk JA, Day CH, Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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Pred. No. 1.3e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       879
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 Kalos MD;
Carter D;
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RESULT 11
AAM79829
ID AAM79829
ID AAM79829
AC AAM79
XX O6-NC
XX Humar
XX Humar
XX Homo
XX Homo
XX Homo
XX O9-AL
XX O9-AL
XX O9-AL
XX O1-FI
PR 27-AI
PR 19-JI
PR 119-JI
PR 20-JI
PR 101-SI
PR 20-JI
PR 101-SI
P
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27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatme of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                     Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer -
                                                                                     Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2;
The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                             WPI; 2001-476283/51.
N-PSDB; AAK52962.
                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM79829 standard;
                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 WKMKPRRNLEEDDYL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100 les 15; Conservative
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                                                                                                                                                                                                                                                S,
                                          20; Page 350; 6221pp; English.
                                                                                                                                                                                                                         Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 879; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA;
                                                                                                                                                                                                                                                                                                                                                                 2000US-0496914.

2000US-0560875.

2000US-0598075.

2000US-0620325.

2000US-0654936.

2000US-0653251.

2000US-0693325.

2000US-0728422.
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                                                                                                                                                                                                                           Drmanac RT, Asundi V, Wang J, Zhang J, Rower Wejhrman T, Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86; DB
Pred. No. 1.3
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepler WT,
                                                                                                                                                                                                                                                                 Asundi V,
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                                                                                                                                                                                                                             Ren
ch R;
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                                                                                                                                                                                                                                                Zhou
F, (
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                                                                                                                                                                                                                                  u C,
Wang
                                                                                                                activities
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                                                                                                                                                                                                                                                   Cao Y,
ng ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE02780 standard;
                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 7p22.3; pancreatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were missing at the time of publication
                                                                                                                                                                               Domain
                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                /label=
                                                                                                           /label= Transmembrane_domain #6
                                                                                                                                     /label= HLA-A2_binding_peptide #3
                                                                                                                                                                                                                                                                                                                                  /label= HLA-A2_binding_peptide #2
                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                            58..166
                                                                                                                                                              label= Transmembrane_domain #5
                                                                                                                                                                                         abel = Transmembrane_domain
                                                                                                                                                                                                                                                                               .abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                310
                                                                                                                                                                                                                      = HLA-A2_binding_peptide #1
                                                     "Encoded by TTGTAGAAT"
                                                                                                                                                                                                                                                                            HLA-A2_binding_peptide #5
                                                                                HLA-A2_binding_peptide
                                                                                                                                                                                                                                                Transmembrane_domain #3
                                                                                                                                                                                                                                                                                                        Transmembrane_domain #2
                                                                                                                                                                                                                                                                                                                                                             Transmembrane_domain #1
                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic_peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 22;
Pred. No. 1.4e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2111 (AAK52582) and 3666 from the sequence listing
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RESULT 13
AAY11840
ID AAY11
XX AA711
XX 18-JU
DT 18-JU
DT 18-JU
DE Human
XX Human
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX 18-FE
XX 11-FE
XX 31-Jt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human six transmembrane epithelial antigen of CC the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell CC surface serpentine transmembrane antigens. STEAP-1 gene is located on CC chromosome 792-3 and is used in gene therapy. Inhibiting the development CC or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian CC and pancreatic) expressing STEAP or inhibiting growth or killing cells CC expressing STEAP in a patient. Treating a patient with a cancer that CC composition to the patient. Treating a patient with a cancer that CC expresses STEAP, or inhibiting growth or killing cells expressing STEAP, CC comprises administering to the patient a vector encoding single chain CC comprises administering to the patient a vector encoding single chain CC comprises administering to the patient a vector encoding single chain CC comprises that the vector delivers the variable domains of the heavy and CC such that the vector delivers the single chain monoclonal antibody coding CC sequence to the cancer cells and the encoded single chain monoclonal CC antibody is expressed intracellularly.

CC Note: The present sequence is also shown in sequence listing of the specification, but it lacks amino acid residues at its N-terminal end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 15
                                                                                                                                                                                  Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                               Human 5' EST secreted protein SEQ ID No: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-367804/38.
N-PSDB; AAD07067.
                       31-JUL-1998;
                                                                                              WO9906550-A2
                                                                                                                                                                     thrombolytic;
                                                                                                                                                                                                                                                                                                                                        18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                        AAY11840;
                                                                                                                                                                                                                                                                                                                                                                                                               AAY11840 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 1A-1B; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New STEAP (six transmembrane epithelial antigen of the prostate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-2000; 2000WO-US33040
                                                         11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 WKMKPRRNLBEDDYL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WKMKPRRNLEEDDYL 15
                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 86; DB 22; illarity 100.0%; Pred. No. 1.4e-06; Conservative 0; Mismarch-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                     anti-inflammatory; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0455486
                       98WO-IB01232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saffran DC,
                                                                                                                                                                       inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc human secreted proteins expressed in prostate, and encode the proteins cg jven in AAY11716 to AAY1193 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene cc products. They can also be used to develop products for diagnosis and ctherapy. The proteins obtained may have cyrokine activity, cell composite and ctivity, tissue growth regulating activity, reproductive hormone cregulating activity, chemotactic/chemotinetic activity, haemostatic and chromobolytic activity, receptor/ligand activity, anti-inflammatory can be used in forensic, gene therapy and chromosome mapping proceduces. The sequences can also be used for obtaining corresponding promoter concerning extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
             Cate RL,
                                                                                                                                                                                                                                     KIM; tissue growth pacute renal failure;
                                                                                                                                                                                                                                                                                                                        01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                       AAW86309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 34; Page 577; 675pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX40562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A, Dumas Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1997;
                                                                                                                                                                           WO9853071-A1
                                                                                                                                                                                                                                   Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                            Kidney injury associated molecule HW018 protein
                                                                                                                                                                                                                                                                                                                                                                                    AAW86309 standard; Protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-153780/13.
                                            (BIOJ ) BIOGEN INC.
                                                                        23-MAY-1997;
                                                                                      23-MAY-1997;
                                                                                                                   22-MAY-1998;
                                                                                                                                                26-NOV-1998
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               Hession CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.4%; Score 70; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                       97US-0047491
97US-0047490
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                                                                                                                   98WO-US10547
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                Sanicola-Nadel M,
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1999-045312/04.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
               Drmanac RT, Liu C,
                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #25508.
                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG25517 standard; Protein; 72 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a kidney injury associated molecule (KIM) protein. KIM proteins can be administered therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 57-58; 213pp; English.
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                                                                                                                                                                                  11-OCT-2001.
                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 WKMKPKGNLEDDSY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA;
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71.4%;
             Tang YT;
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2; Mismatches
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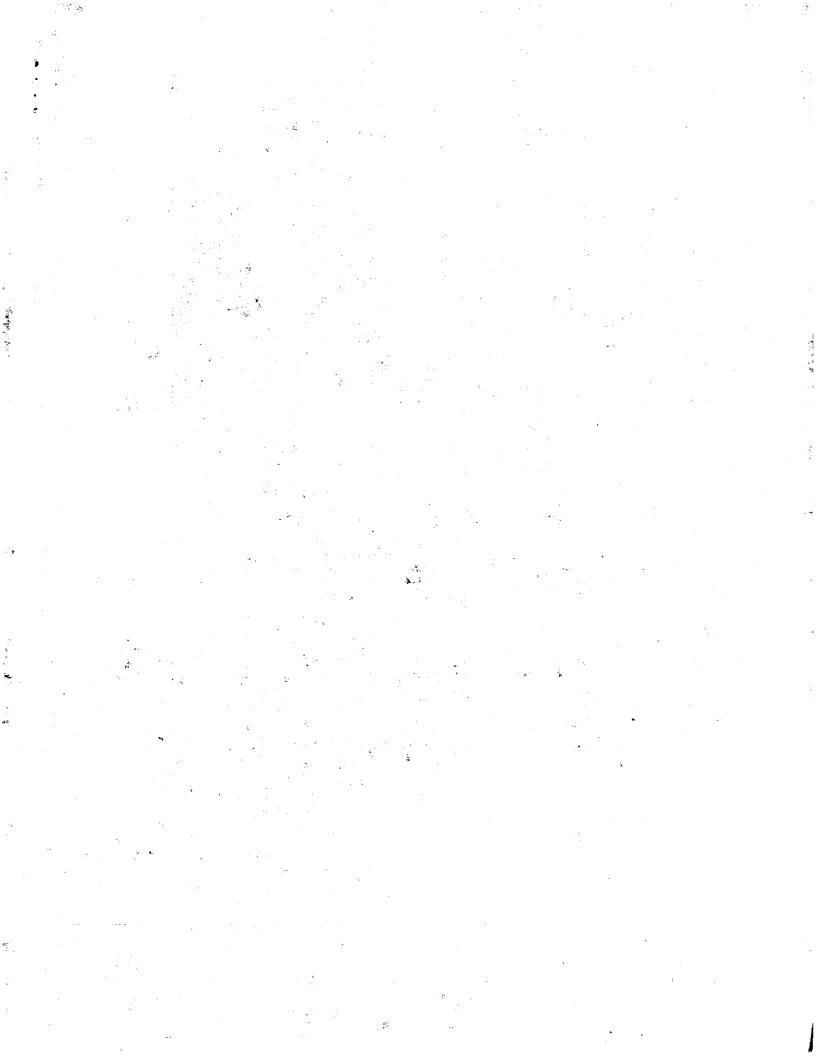
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymelectides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed case for the patent of the printed control of the control of the control of the printed control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 55876; 103pp; English
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N-PSDB; AAS89704.
                                                                        at ftp.wipo.int/pub/published_pct_sequences.
72 AA;
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밁 Ś Query Match
Best Local Similarity
7; Conserv 39 WKLKPONNLPE 49 1 WKMKPRRNLEE 11 Conservative 52.3%; 2; Mismatches Score 45; 1 Pred. No. 3 DB 22; 3.1; 2; Length 72 Indels 0, Gaps

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Search completed: March 26, 2003, 16:48:00 Job time : 33.1279 secs



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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     38
37.5
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6 NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6 NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                   Match
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   339
1018
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                               US-10-012-896-879
US-09-802-520-11
US-09-895-793-879
US-09-895-814-879
US-10-011-095-2
US-10-010-6678-2
US-10-016-678-2
US-10-016-678-879
US-09-759-143-879
US-09-813-574-76
US-09-813-4534-12
US-09-813-4534-12
US-09-813-4534-12
US-09-813-4536-7348-12
US-09-813-232-10497
US-09-813-242-10497
US-09-813-242-10497
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                    US-09-759-010-7
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Sequence 879, App
Sequence 879, App
Sequence 879, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 879, App
Sequence 45, Appl
Sequence 45, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 75, Appl
Sequence 7, Appli
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Sequence 160, App Sequence 160	18, 14, 66, 61, 160,

ALIGNMENTS

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APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITITLE OF INVENTION: COMPOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
; ORGANISM: Homo sapiens US-10-012-896-879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-012-896-879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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McNeill, Patricia D.
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Hepler, William T.
Henderson, Robert A.
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Mitcham, Jennifer L.
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Vinals de Bassols, Carlota
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Carter, Darrick
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9.5e-07;

DB 9;

Length 339;

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; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SOPTWARE: PERL Program
SEQ ID NO 11
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Homo mapiens
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Craig H.
                       APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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APPLICANT: Dillon, Davin C.
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CURRENT APPLICATION
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Kalos, Michael D.
                                                                                          McNeill, Patricia D.
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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                                                                           Foy, Teresa
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Carter, Darrick
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o. US20020192763A1
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ilarity 100.0%; Pred. No. 9.:
Conservative 0; Mismatches
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NUMBER: US/09/895,793
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-879
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APPLICANT: Foy, Teresa
APPLICANT: POY, Teresa
APPLICANTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FAPPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 879
SEQ ID NO 879
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NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 879
LENGTH: 339
                                                                Matches
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                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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14 WKMKPRRNLEEDDYL
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                   1 WKMKPRRNLEEDDYL 15
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Dillon, Davin C.
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Kalos, Michael D.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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                                                                100.0%; ilarity 100.0%; Conservative 0
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ick, Thomas S.
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                                                                                Score 86; DB 9;
Pred. No. 9.5e-07;
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Pred. No. 9.5e-07;
                                                                   Mismatches
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                                                                                                Length 339;
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RESULT 5
US-10-011-095-2
; Sequence 2, Application US/10011095
; Publication No. US20030045682A1
; GENERAL INFORMATION:

APPLICANT: Afar, Daniel

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APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR PILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR PILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                            Query Match
Best Local :
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                                                                                       Matches
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APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rend
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Ari
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                        LENGTH: 339
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                         WKMKPRRNLEEDDYL 15
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Leong, Kahan
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                                                                                                         100.0%; Score 86; DB 9; 100.0%; Pred. No. 9.5e-07;
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                                                                                       Mismatches
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION UMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: SECEN 620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for W:
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
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o. US20020022248A1
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Carter, Darrick
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Vedvick, Thomas S.
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Kalos, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craig H.
ick, Thomas S.
                                                                                                                                                                                                                                                                                                                          Tugut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 86; DB 10; 100.0%; Pred. No. 9.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Susan L.
                                                                                                                                                                                                                                                                                                               Robert A.
                                                                                                                                                                                                                                                                                                                                             Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert A.
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                                                      THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 339;
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CURRENT FILING DATE: 200

NUMBER OF SEQ ID NOS: 94

SOFTWARE: FastSEQ for Wi

SEQ ID NO 879

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens
US-09-780-669-879
                                                                     ; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-801-574-32
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOPTMARE: FRACEGO for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 86;
Matches 15; Conservative 0; Mismatch
                                                                                                                                            SOFTWARE: FO
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/09801574 Patent No. US20020081592A1
                Query Match
Best Local Similarity
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 Matches
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
FRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 WKMKPRRNLEEDDYL 28
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                                                                                                                                                             FastSEQ for Windows Version
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Conservative
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                48.8%;
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Score 42; DB 10; Length 1018;
Pred. No. 73;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; I
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RESULT 13 US-09-486-734A-12 ; Sequence 12, Application US/09486734A

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GENERAL INFORMATION:

APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.

TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR APPLICATION NUMBER: 60/261,557
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/227,860
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/667,569
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 45
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-76
                                                 Query Match
Best Local Similarity
Friches 6; Conserve
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US-09-801-574-76
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                                                                                                                                     ; TYPE: PRT; ORGANISM: Bacillus anthracis
US-09-813-453A-45
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/09801574 Patent No. US20020081592A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/09813453A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PATTERSON, THOMAS A.
TITLE OF INVENTION: MICROORGANISMS AND ASSAYS
TITLE OF INVENTION: ANTIBIOTICS
FILE REFERENCE: OGZ-001
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yocum, R. Rogers APPLICANT: Patterson, Thoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       646
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26
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                               1 WKMKPRRNLEEDDY 14
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WRMETDRHKTEDEY 39
                                                                 Conservative
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Pred. No.
                                                                                   Score 39;
Pred. No.
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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74;
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                                                                                                   Length 262
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                                                                     Indels
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                                                                   Gaps
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APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
APPLICANT: Institut National de la Recherche Agronomique
ITILE OF INVENTION: Resistance Mechanisms to Ic Type R/M
ITILE OF INVENTION: Bacteriaphages of Lactic Acid Bacteria
FILE REFERENCE: 33339/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/FR98/01873
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEO ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 404
TYPE: PRT
ORGANISM: Lactococcus lactis
; ORGANISM: Enterococcus faecalis US-09-815-242-10497
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                                                                                                                                                              PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.2%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10497
LENGTH: 539
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick, John D.
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                                                                                                                     for Windows Version 4.0
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Pred. No. 1.2e+0;
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RESULT 15

US-09-753-008-7

I Sequence 7, Application US/09753008

PARENT NO. US20020061520A1

GENERAL INFORMATION:
APPLICANT: Stefan Somlo and Toshio Mochizuki
                                                                      Query Match
Best Local Similarity
""" hes 6; Conserve
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Best Local S
Matches
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  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 02-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/385,752
PILING DATE: 1999-08-30
APPLICATION NUMBER: 08/651,999
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTIER TOOMS

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1

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DISKETTE

DISKETTE
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                                                 1 WKMKPRRNLEEDD 13
                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,008
                                                                                                                                                                                                                         HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO:
WKMOPSNOTEADN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
7; Conserv
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STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                     DESCRIPTION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/395
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 968 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
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                                                                                                  Conservative
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                                                                                               44.2%; Score 38; DB 10;
46.2%; Pred. No. 3.2e+02;
ative 2; Mismatches 5
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Pred. No. 1.7e+02;
                                                                                                                                                 DB 10; Length 968;
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Search completed: March 26, 2003, 17:04:14 Job time : 11.1163 secs

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Maximum Match 100%
Listing first 45 summaries
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    SPTREMBL 2

1: sp_arch
2: sp_bac
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86
1 WKMKPRRNLEEDDYL 15
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196.889 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	Q	ហ	4.	w	N	_	Result No.
42	43	43	43	44	44	44	44	45	45	45.5	63	63	63	67.5	78	Score
48.8	50.0	50.0	50.0	51.2	51.2	51.2	51.2	52.3	52.3	52.9	73.3	73.3	73.3	78.5	90.7	Query Match
124	679	398	312	773	659	532	317	2058	375	237	339	339	339	338	264	Query Match Length DB
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Q928f4 listeria in	Q98856 cynops pyrr	Q94hs8 oryza sativ	Q17557 caenorhabdi	Q91uq5 rhizobium m	076517 trypanosoma	O80941 arabidopsis	O96654 trypanosoma	Q91gg0 oryza sativ	· Q8xdr7 escherichia	Q9uta5 schizosacch	Q924j9 mus musculu	Q924z2 mus musculu	Q9cwr7 mus musculu	Q9g150 sus scrofa	Q9y6u5 homo sapien	Description

ALIGNMENTS

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RESULT 1

Q9Y6U5

ID Q9Y6U5

PRELIMINARY; PRT; 264 AA.

AC Q9Y6U5;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence)

DB WUGSC:H_RG087E15.1 protein (Fragment).

GN WUGSC:H_RG087E15.1 protein (Fragment).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; But MuGSC:H_RG087E15.1.

OC Hammalia; Butheria; Primates; Catarrhini; Hominidae; HC Mammalia; Butheria; PubMed=9847074;

RN SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

MEDIJINE-99066; _
RT "Toward a complete human genome sequence.";

RA SIISton J.E., Waterston R.;

RY "Toward a complete human genome sequence.";

RA SIISton J.E., Waterston R.;

RY "Toward a complete human genome sequence.";

RA SECOUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA Waterston R.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AC005061; AAD43182.1; -.

FT NON_TER

264

SEQUENCE 264 AA; 31203 NM; 35C9483003557E72 CRC64;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005061; AAD43182.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             Strong C., Layman D., Graves T., Strowmatt C.; "The sequence of Homo sapiens BAC clone CTB-87E15."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
1 WKMKPRRNLEEDDYL 15
                                                                              13;
                                                                              Similarity 86.7
13; Conservative
                                                                                                   90.7%;
86.7%;
                                                                              2;
                                                                                                        Score 78; DB 4; Length 264; Pred. No. 1.7e-05;
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RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsudi F., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,

Raskai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Raskai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Raskai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Raskai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Raskai K., Okido T., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D.,

Raskai K., Okido T., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D.,

Raskai K., Okido T., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D., Furuno M., Aono H., Saninci M.,

Raskai K., Okido T., Furuno M., Aono H., Saninci D., Furuno M., Aono H., Saninci M., 
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Q9CWR7;
01-JUN-2001 (
01-JUN-2001 (
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Q9GL50;
01-MAR-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
51x transmembrane endothelial antigen of PAEC.
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE-EMBRYONIC STEM CELLS; MEDLINE-21085660; PubMed-11217851;
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STEAP OR 2410007B19RIK.
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Mammalia; Eutheria;
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Heslan J.-M., Soulillou J.-P.,
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                                  "Functional annotation of a Nature 409:685-690(2001).
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Rodentia;
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Pred. No. 0
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                                                                        mouse cDNA collection.";
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
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01-DEC-2001
01-DEC-2001
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SEQUENCE FROM N.A.

STRAIN=C57BL/6;

STRAIN=C57BL/6;

STRAIN=C57BL/6;

MEDLINE=21371909; PubMed=11479226;

Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;

Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;

Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;

Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;

Yang D., Ka
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SEQUENCE 339 AA; 3926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of human STEAP.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AY029584; AKK50537.1;
MGD; MGI:1915678; 1010001D01Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q924Z2
                                                                                                             transgenic adenocarcinoma mouse prostate Cancer Res. 61:5857-5860(2001).
EMBL; AF297098; AAK83126.1; -.
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   Transmembrane.
                                                                          EMBL; AF297098; AAK83126
MGD; MGI:1917608; Steap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q924J9;
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Serru V., Manivet
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(TrEMBLrel.
2 (TrEMBLrel.
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(TrEMBLrel. 19, L
(TrEMBLrel. 21, L
mbrane epithelial
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Rodentia;
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Rodentia;
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       39318
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71.4%;
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       XE.
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Last annotation update)
I antigen of the prostate.
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vert
Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32A2C29F2E333BD0 CRC64;
       4B26A71FF559E84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Mus.
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DB 11; Length 339;

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RESULT 7
QBXDD AC QBXD
DT Q1-M
DT Q1-M
DT Q1-M
DT Q1-M
DT Q1-J
DE RNas
GN RND
OS Esch
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OBXDR7;

OHMAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

RNase D, processes tRNA precursor.

RNB OR Z2847 OR ECS2513.

Therichia coli O157:H7.

Therichia coli O157:H7.
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Barrell B.G., Rajandream M.A., McDougall R.C., McLean J., Harris
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133225; CAB61781.1; -.
InterPro; IPR003827; DUF207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9UTA5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                 STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=1120551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Apodaca J., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein. SPAC25B8.15C.
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MEDLINE=21156231; PubMed=11258796; Hayashi T., Makino K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=83334;
                                                                                                                                                                   "Genome sequence of enterohaemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 RMKPRRKLRNMDDYL 234
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71.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.5;
Pred. No. 6.
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          Kurokawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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          Ishii K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 237;
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                                                                                                                                                                   coli 0157:H7.";
             Yokoyama K.,
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096654
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Best Local Similarity
Watches 7; Conserve
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Best Local Similarity
                                                                                                       O96654 PRELIMINARY;
O96654;
O1-MAY-1999 (TrEMBLrel. 10, C
O1-MAY-1999 (TrEMBLrel. 20, L
O1-MAR-2002 (TrEMBLrel. 20, L
Activated protein kinase C re
Trypanosoma vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LGGO;
01-0CT-2000 (TrEMBLr:
01-0CT-2000 (TrEMBLr:
01-DEC-2001 (TrEMBLr:
P0406H10.14 protein.
P0406H10.14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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EMBL; AP002558; BAB35936.1; -.
InterPro; IPR002562; 3 5 exonuclease.
InterPro; IPR002121; HRDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002524; BAB07964.1; -. SEQUENCE 2058 AA; 226376 MW; BA06B6562B8BBD69 CRC64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00474; 35EXOC; 1.
SMART; SM00341; HRDC; 1.
                 SEQUENCE FROM N.A.
                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone: P0406H10."
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Pfam; PF00570; HRDC; 1.
STRAIN=ILDAT1.2;
                                                                 NCBI_TaxID=5699;
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L (TrEMBLrel.
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                                                                                                                                        receptor homolog.
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Last annotation updat
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Pred. No.
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Pred. No.
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83;
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Best Local S
Matches 10
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Best Local Similarity
Matches 7; Conserv
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O80941;
O80941;
O1-NOV-1998 (TrEMBLrel. 08, C)
O1-NOV-1998 (TrEMBLrel. 08, L)
O1-DEC-2001 (TrEMBLrel. 19, L)
At2937730 protein.
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ProDom; PD000018; WD40; 4.

SMART; SM00320; WD40; 7.

PROSITE; PS00678; WD REPEATS 1; UNKNOWN_3.

PROSITE; PS50082; WD REPEATS 2; 5.

PROSITE; PS50082; WD REPEATS REGION; 1.

Kinase; Receptor; Repeat; WD repeat.

Kinase; Receptor; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Pujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
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EMBL; AF100287; AAC72850.1; --
Interpro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC004684; AAC23643.1; -. SEQUENCE 532 AA; 60372 MW; 157066866846B4E5 CRC64;
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STRAIN=CV. COLUMBIA;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN=CV. COLUMBIA;
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Q1-DEC-2001
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Plasmid.
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Mol. Biochem. Parasitol. 98:17-28(1999).

Mol. Biochem. Parasitol. 98:17-28(1999).

EMBL; AF074867; AAC28456.1; -.

InterPro; IPR001064; Crystallin.

PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN 1.

PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN 1.
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MEDLINB=99151764; PubMed=10029306;
Kelley R.J., Alexander D.L., Cowan C.,
"Molecular cloning of p67, a lysosomal
"Trypanosoma brucei.";
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Lysosomal/endosomal membrane protein p67.
Trypanosoma brucei rhodesiense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residing in the rhizosphere of alfalfa.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AJ304453; CAC79182.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genetic organization and evolution of the broad-host-ramercury resistance plasmid pSB102 isolated from a microbial residing in the rhizosphere of alfalfa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718; Schneiker S., Keller M., Droege M., Lanka E., Pu
Selbitschka W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pSB102.
Bacteria, Proteobacteria,
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NCBI_TaxID=31286;
                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR000380; Prok_tpisomrase
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Sinorhizobium.
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01-NOV-1996 (TrEMBLrel. 01, I
01-DEC-2001 (TrEMBLrel. 19, I
COLF1.2 protein.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Pulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McChurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1996) to the EMBL/GenBank/DDBU databases.
EMBL; U58761; AAB00716.1; -.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000566; Lipocln cytFABP.
InterPro; IPR003782; SC01_SenC.
Pfam; PF02630; SC01_SenC.
SMART; SM00012; PTPC_DSPC; 1.
PROSITE; PR00213; LIPOCALIN; UNKNOWN 1.
SRQUENCE 312 AA; 35650 MW; 943AB533E88ECDA5 CRC64;
                                                                                                  Hypothetical protein.
Oryza sativa (Rice).
Cryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae;
  SEQUENCE FROM N.A. Wing R.A., Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid C01F1.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00041; hemopexin; 4.
Pfam; PF00413; Peptidasee M10; 1.
Pfam; PF00413; PATTYPEII.
PRINTS; PR00113; MATRIXIN.
PRODOM; PD000195; FN Type_II; 3.
SMART; SM00059; FN2; 3.
SMART; SM00025; FN2; 4.
SMART; SM00236; CYSTEINE SWITCH;
PROSITE; PS00023; FIBRONECTIN 2; 3.
PROSITE; PS00023; FIBRONECTIN 2; 3.
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Q98856;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-FEB-1997 (TrEMBLrel. 19, Last sequence update)
Q1-FEB-1997 (TrEMBLrel. 19, Last annotation update)
Q1-FEB-1997 (TrEMBLrel. 19, Last annotation update)
Q1-FEB-1997 (TrEMBLrel. 19, Last annotation update)
Q2 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase-B).
Cynops pyrrhogaster (Japanese common newt).

Cynops pyrrhogaster (Japanese common newt).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of regenerating newt limbs.";
Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
BE INVOLVED IN TISSUE REMODELLING OF THE REGENERATING LIMB.
PROC. CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPES I AND V AND COLLAGION.
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                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.; "Cloning and characterization of cDNAs for matrix metalloproteinases
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   Collagen degradation;
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InterPro: IPR000585; Hemopexin.
InterPro: IPR001818; Matrixin.
InterPro: IPR000130; Zn_MTpeptdse.
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MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN B
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SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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PS00546; CYSTEINE SWITCH; 1.
PS00023; FIBRONECTIN 2; 3.
PS00024; HEMOPEXIN; I.
PS000142; ZINC PROTEASE; UNKNOWN 1.
PS000142; ZINC PROTEASE; UNKNOWN 1.
Ce; Metalloprotease; Glycoprotein; Zinc; Zymo
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PT CHAIN 28 105 AUTOINHIBITOR REGION.

PT DOMAIN 282 339 FIBRONECTIN TYPE-II.

PT DOMAIN 340 397 FIBRONECTIN TYPE-II.

PT DOMAIN 486 679 FIBRONECTIN TYPE-II.

PT DOMAIN 401 401 ZIMC (CAPALYTIC) (BY SIMILARITY).

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PT ACT_SITE 402 402 ENG. (CAPALYTIC) (BY SIMILARITY).

PT ACT_SITE 401 401 ENG. (CAPALYTIC) (BY SIMILARITY).

PT ACT_SITE 402 ENG. .) (POTENTIAL).

SO SEQUENCE 679 AA; 75581 MW; 573CDDB9DBF85524 CRC64;

Query Match 8; Score 43; DB 13; Length 679;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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AF186249; AC005053; AC004969; BC011802; ; HGNC:1137; 604415;	the Swiss yean Bioinf non-profit and this s requires an nemail to	FROM N.A. deh J., S (JUN-199 FROM N.A. in; g R.; g R.; l (JUL-200 E JUL-200 E SPECIFI	SEQUENCE FROM N.A. MEDLINB=20056277; Hubert R.S., Vivan Mitchell S.C., Mad Jakobovits A., Saf "STEAP: a prostate human prostate tum Proc. Natl. Acad.	STEA HUMAN STANI GSULES; 095034; [09HLE8; 095034; [16-OCT-2001 (Rel. 4C) 16-OCT-2002 (Rel. 4C) 15-JUN-2002 (Rel. 4C) 15-SIX transmembrane eg STEAP OR STEAP1. HOmo sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; MCBI TaxID=9606;		44444444444444444444444444444444444444
AAF17479.1; AAC79150.1; AAD15620.1; AAH11802.1; 78; STEAP.	s SWISS-PROT entry is copy ween the Swiss Institute European Bioinformatics by non-profit institut by non-profit institut ified and this statement ities requires a license a send an email to licensee	Abu-Threideh J., Stoneking Abu-Threideh J., Stoneking Submitted (JUN-1998) to th [3] SEQUENCE FROM N.A. TISSUE-Skin; Strausberg R.; Strausberg R.; Strausberg R.; STRAUSCELLULAR LOCATION: -!- TISSUE SPECIFICITY: HI				1371 3866 3969 7916 802 803 133 133 136 230
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P09155;
01-MAR-1989
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Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
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corresponding to the 40.1-50.0 min region on the linkage map.";
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
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"Escherichia coli RNase D: sequencing of the
purification of the overexpressed protein.";
Nucleic Acids Res. 16:6265-6278(1988).
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01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Ribonuclease D (EC 3.1.26.3) (RNase D).
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                                                                                                                                               AMP-binding protein family.";
Mol. Gen. Genet. 242:241-249(1994).
-i- FUNCTION: CLEANES MULTIMERIC TRNA PRECURSOR AT THE
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                         Fulda M., Heinz E., Wolter F.P.;
"The fadD gene of Escherichia coli K12 is located close 39.6 min of the chromosomal map and is a new member of t
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SUBCELLULAR LOCATION: Cytoplasmic.
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InterPro; IPR002121; HRDC.
Pfam; PF00570; HRDC; 1.
Pfam; PF01612; 3_5_exonuclease; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00341; HRDC; 1.
                                              PFAM; PP00765; Autoind synth; 1.
PRINTS; PR01549; AUTOINDCRSYN.
PRODOR; PD002752; Autoind synth; 1.
PROSITE; PS00949; AUTOINDCERS SYNTH;
Quorum sensing; Autoinducer synthesis
SEQUENCE 193 AA; 22127 MW; 238E760
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxodecanoyl)-L-homoserine lactone.";
J. Bacteriol. 179:3004-3012(1997).
-i- FUNCTION: REQUIRED FOR THE SYNTHE
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Milton D.L., Hardman A., Camara M., Chhabra S.R.,
Stewart G.S.A.B., Williams P.;
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or send an email to license@isb-sib.ch).
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vanI/vanR locus and identification of the autoinducer N-(3-
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RA Sgouros J., Peat N., Hayles J., Bakker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Commor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Commor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDenn J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mitherford K., Rutter S., Saunders D., Geeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonpres B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Rainhardt R., Purnelle B.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lehaure V., Mottier S.,
RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT "He genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                014283; Q9UTX5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor prri (Pombe response regulator 1).
PRR1 OR SPAC8C9.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPO
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MEDLINE=99279565; PubMed=10348908;

MEDLINE=99279565; PubMed=10348908;

MEDLINE=99279565; PubMed=10348908;

Major T.;

                                                                                                 "Large-scale screening of intracellular protein localization fission yeast cells by the use of a GFP-fusion genomic DNA li Genes Cells 5:169-190(2000).

-I- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACACTS UPON TRR1 AND CTT1.
                                                                                                                                                                                                                                                                                                              Ding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRR1
                                                                                                                                                                                                                                                                                                                                               MEDLINE=20223868;
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=968 h90;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 224-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHPO
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                                                                                                                                                                                                                                                                                                                     Tomita
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                                                                                                                                                                                                                                                                                                              PubMed=10759889;
Y., Yamamoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                              Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539
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                                       THE HSF FAMILY
                                                                                                                                                                                                             DNA library.";
                                                                                                                                                FACTOR THAT
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RESULT
ODP2_BA
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Best Local
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component complex (EC 2.3.1.12) (E2) (S complex, 48 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00434; HSF DOMAIN; 1.
PROSITE; PS50110; RESPONSE REGULATORY; 1.
Transcription regulation; Sensory transduction; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00056; HSFDOMAIN.

Prodom; PD000039; Response reg;
Prodom; PD001788; HSF DNA Dind;
SMART; SM00415; HSF; I.

SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB027943; BAA87247.1; -.
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                                                                                                                                                                                                                                                                                                   Hemila H., Palva A., Paulin L., Arvidson S., "Secretory S complex of Bacillus subtilis: se identity to pyruvate dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P21883;
SEQUENCE FROM N.A.
                                                                        Winters P., Caldwell R., Enfield L., Ferrari E.; "The ampS-nprE (124 degrees-127 degrees) region of the subtilis 168 chromosome: sequencing of a 27 kb segment identification of several genes in the area.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Phosphorylation.
                                             Microbiology 142:3033-3037(1996)
                                                                                                                                                                        MEDLINE=97124187; PubMed=8969500;
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90368558; PubMed=1697575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002341; HSF_ETS.
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR000232; HSF_DNA_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 WKROPRILLVEDDEL 378
                                                                                                                                                                                                                                                                                   Bacteriol.
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9; Conserv
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418
539 AA;
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                                                                                                                                                                                                                                                                                   172:5052-5063(1990).
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418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillales;
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Pred. No.
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PHOSPHORYLATION (BY
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F3B4945C595B2871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                sequence analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Length 539;
                                                                                                                                                                                                                                                                                                                                                              Palva I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of pyruvate dehydrogenase subunit).
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RESULT
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Best Local S
Matches 7
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SubtiList; BG10209; pdhC.
SubtiList; BG10209; pdhC.
InterPro; IPR001078; 20xoacid dh.
InterPro; IPR001078; Biotin lipoyl.
InterPro; IPR004167; E3_binding.
InterPro; IPR003016; Lipoyl.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin lipoyl; 1.
Pfam; PF02817; e3_binding; 1.
PROSITE; PS001189; LIPOYL; 1.
PROSITE; PS00189; LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome.";
Submitted (JUI.-100)
                                                                                                                    AGUA_TRIRE
Q99074;
Q99074;
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
ACT_SITE
SEQUENCE
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INIT MET
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                        Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M57435; AAA62463.1; -.
EMBL; AF012265; AAC24934.1; -.
EMBL; Z99111; CAB13333.1; -.
EMBL; D36718; D36718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through
                                                                                             Alpha-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caldwell R.M.,
    Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                            (GLRI)
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                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrollpoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

PUNCTION: THE B.SUBTILIS PDH COMPLEX POSSESSES ALSO BRANCHED-CHAIN 2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: The pyruvate dehydrogenase complex catalyzes the conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: FORMS A 24-POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acetyldihydrolipoamide.
COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYMMETRY
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                                                                                                                                                                                                                                                                                                                                        WFVKPNDEVDEDDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 AA;
                                                                                             (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last snotation update)
ronidase precursor (EC 3.2.1.139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Acyltransferase; Lipoyl; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
42
412
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
    Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrari E.;
vsis of the mobA-ampS region of the
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
181
42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%;
                                                                                                                                                                                                                                                                                                                                                                                     15
    Hypocrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPOYL BINDING.
E1/E3 BINDING.
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6B44D47879D134DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURAL
                                                                                                                                                                                                                      847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                (Alpha-glucosiduronase)
                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                             Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by and
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tent is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCTAHEDRAL
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CCCCCCRRRRRRR OOCOGETTTE
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ST31_MC
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                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                               Q99MWI;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03648; Gly(
Xylan degradation;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96257277; PubMed=8654984; Margolles-Clark E., Saloheimo M., "The alpha-glucuronidase-encoding Gene 172:171-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                         MEDLINE=21175748; PubMed=11279525; Wang P.J., McCarrey J.R., Yang F., Page D.C.; "An abundance of X-linked genes expressed in a standance of X-linked genes expressed in Nat. Genet. 27.422-426 (2001).

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP -i- TISSUE SPECIFICITY: Testis-specific. Expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                     Serine/threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=QM9414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=51453;
                                                                                                              rissuE=Testis;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                         2 KMKPRRNLEEDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + D-glucuronate
SUBCELLULAR LOCATION: Secreted
SIMILARITY: BELONGS TO FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RELEASES 4-O-METHYLGLUCURONIC ACID CATALYTIC ACTIVITY: An alpha-D-glucuronoside
         SIMILARITY: BELONGS TO THE SER/THR FAMILY OF SIMILARITY: CONTAINS 1 TUDOR DOMAIN.
                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                    KLSPKINIKEDGY
                                                                                                                                                                                                                                                                                                                                                             7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR005154; Glyco_hydro_67.
3648; Glyco_hydro_67; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        767
847
                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                20
238
321
353
586
692
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                     protein
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321
353
586
592
                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                          48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drolase;
                                                                                                                                                                                                     kinase 31
                                                                                                                                                                                                                                                                                                                                                                                                           ME;
                                                                                                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-GLUCURONIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosidase;
                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                            214AAE487382FDB4
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siika-Aho M., Penttilae M.;
gene of Trichoderma reesei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                     (E)
                                                                                                                                                                                                                                                              1018
                                                                                                                                                                                                     update)
C 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC.
                                          = ADP + a phosphoprotein.
Expressed only in male g
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                                                                                                                                                                                                                                                                                                                                                                                      μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                            spermatogonia.";
                                                                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                                                                    Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM XYLAN:
+ H(2)O = a
                       PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                            male germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an alcohol
                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                              Gaps
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN STANDARD; PRT; 1019 AA.

(OBENÜI; OSEXHB;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Serine/threonine protein kinase 31 (EC 2.7.1.37) (Serine/threonine-protein kinase NYD-SPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP BIND
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 1.
Pfam; PF00567; TUDOR; 1.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S TKC; 1.
SMART; SM00333; TÜDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as great as its content is in no modified and this statement is not removed. Usage by and for comment entities requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
development.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP
-!- TISSUE SPECIFICITY: Testis-specific
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
-!- SIMILARITY: CONTAINS 1 TUDOR DOMAIN.
                                                                                                                         Zhou
                                                                                                                                                                                                                                                                                                                                                                                              STK31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50011; PROTEIN KINASE_DOM; 1. PROSITE; PS50304; TUDOR; 1.
                                                                                      "Cloning of a new
                                                                                                                                                            SEQUENCE OF 24-1019
                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                              MEDLINE=21175748; PubMed=11279525;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1924735; Stk31
                                                                                                                                           TISSUE=Testis;
                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WKMKPRRNLEEDD 13
                                                                                                                                                                                           g P.J., McCarrey J.R., Yang F., Page D
abundance of X-linked genes expressed
. Genet. 27:422-426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKLVEKSNLEESD 658
                                                                                                                           Z.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF285580; AAK31959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 53.4
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000719; Euk pkinase.
IPR001097; Maternal_tudor.
IPR000080; SNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002290; Ser_thr_pkinase
IPR002999; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1018
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105
298
711
717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine/threonine-protein kinase;
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245
358
1018
725
738
                                                                                                        protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.8%;
                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115027
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TNASE-LIKE.
TNASE-LIKE.
COILED COIL (POTENTIAL
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1206284ED4E90816 CRC64;
                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                          related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                             spermatogonia.";
                                             databases.
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                                                                                                      human testis
                    PROTEIN KINASES
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                                                   phosphoprotein.
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RESULT 9
HTPG TREPA
ID HTPG T
AC 083949
DT 15-DEC
DT 15-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
Matches
                                                                                                                                                                                            HTPG_TREPA STANDARD;

083949;

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-UN-2002 (Rel. 41, Last annotation update)

15-Un-prone protein htpG (Heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
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NP_BIND

BINDING

CONFLICT

CONFLICT
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SMART; SM00220; S_TKC; 1.

SMART; SM00230; TUDOR; 1.

SMART; SM00333; TUDOR; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50304; TUDOR; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to entitles requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase; Pfam; PF00567; TUDOR; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF285599; AAK31978.1; EMBL; AF332194; AAK17193.1;
SEQUENCE FROM N.A.
STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M.,
                                                                                                                                                                           protein G).
HTPG OR TP0984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Serine/threonine-protein Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001097; Maternal tudor.
InterPro; IPR000090; SNase.
InterPro; IPR002290; Ser thr_pkinase.
InterPro; IPR002999; Tudor.
                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                          NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                              645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WKMKPRRNLEEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 53.47; Conservative
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1019
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I -> F (IN REF. 2)

F -> Y (IN REF. 2)

KKI -> NKS (IN REF. 2)

Y -> C (IN REF. 2)

V -> A (IN REF. 2)

K -> I (IN REF. 2)

K -> I (IN REF. 2)

A -> G (IN REF. 2)

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                                                                                                                                  Spirochaetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB
Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.
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                                                                                                                                                                                                              ion update)
protein htpG) (High temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
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      White O.,
                                                                                                                                  Treponema
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        Sutton G.G.,
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Best Local S
Matches 7
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Sodergren E., Hardham
Khalak H., Richardson
McDonald L., Artiach P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HSVMG
ICP4_HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
ICP4.
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Pfam; PF02518; HATPase C; 1.
PR1NTS; PR00775; HEATSHOCK90.
SWART; SW00387; HATPase C; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Treponema spirochete."; Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Trans-acting transcriptional activator protein
protein IEI75).
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                                                                                                                                                     gene.";
Virology 189:657-667(1992).
                                                                                                                                                                                                                      MEDLINE=92351564; PubMed=1322594;
Anderson A.S., Francesconi A., Morgan
"Complete nucleotide sequence of the N
                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
Alphaherpesvirinae; Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marek's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q02362;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaperone; ATP-binding; Heat shock; Complete proteome.
DOMAIN
1 348 A; SUBSTRATE-BINDING (BY
DOMAIN 349 565 B (BY SIMILARITY).
DOMAIN 566 639 C.
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HSSP; P02829; 1AH8.
TIGR; TP0984; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hatch B., Horst K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10388;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
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InterPro; IPR001404; Hsp90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
PUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLI
OF MICRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
OTHER VIRAL GENES, AND AUTORREGULATING ITS OWN SYNTHESIS. IT IS
REQUIRED FOR THE SWITCH FROM IMMEDIATE-EARLY TO EARLY MODE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Molecular chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eimilarity).
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B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Richardson D., Howell J.K., Chidambaram M., Utterback T.,
.., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               herpesvirus (strain GA) (MDHV)
viruses, no RNA stage; Herpesvii
nae; Marek's disease-like viruse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258
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Pred. No. 33;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3E8FDBAC2282C31D
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                                                                                                                                                                                                                             an R.W.;
e Marek's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpesviridae,
ike viruses.
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                                                                                                                                                                                                                             disease virus
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                                                                                                                                                                                                                             ICP4
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RESULT
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Best Local S
Matches
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P30370;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seque
15-JUL-1999 (Rel. 38, Last annot
Retinoic acid-binding protein II
             HSSP; P293
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                       Kitamoto T., Momoi T., Momoi M.;

Biochem. Biophys. Res. Commun. 159:371-371(1989).

-:- FUNCTION: CYTOSOLIC CRABPS MAY REGULATE THE ACCESS OF RETINOIC ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS.

-!- FUNCTION: CRABP-II MAY PARTICIPATE IN A REGULATORY FEEDBACK MECHANISM TO CONTROL THE ACTION OF RETINOIC ACID ON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M75729; AAA46111.1; -.

PIR; A42991; BDBEGA.

InterPro; IPR005205; Herpes_ICP4_C.

InterPro; IPR005205; Herpes_ICP4_N.

Pfam; PF03584; Herpes_ICP4_N; 1.

Pfam; PF03585; Herpes_ICP4_C; 1.

Barly protein; Transcription regulation; Trans-acting DNA-binding; Phosphorylation; Nuclear protein.

DOMAIN

155

200

SER/PRO-RICH.

SER/PRO-RICH.

CRC6
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                                                                                                                                                                                                                                                   MEDLINE=89087453; PubMed=2849937;
Kitamoto T., Momoi T., Momoi M.;
"The presence of a novel cellular retinoic acid-binding protein
chick embryos: purification and partial characterization.";
Biochem. Biophys. Res. Commun. 157:1302-1308(1988).
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                                                    PIR; B31872; B31872.
                                                                                                                                                                                                                            ERRATUM
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 KASPRTRKLEDEDYL
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SUBCELLULAR LOCATION: NUCLEUS
PTM: A LONG STRETCH OF SERINE
PHOSPHORYLATION
                                                                                  TISSUE SPECIFICITY: SIMILARITY: BELONGS
                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                  TRANSPORTERS
                                                                                                                              DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMKPR-RNLEEDDYL
       P29373; 1CBS.
Pro; IPR000463; Fatty acid BP.
Pro; IPR000566; LipocIn_cytFABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
protein II, cellular (CRABP-II) (Fragment).
                                                                                  EMBRYO.
TO THE FABP/P2/CRBP/CRABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.5;
Pred. No. 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1415;
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RESULT 13
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RET3_X
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Best Local Similarity
Matches 7; Conser
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Best Local (
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Vitamin A; Transport.
NON TER 36 36
SEQUENCE 36 AA; 399
                                MAMUH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RET3_XENLA
P50568;
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I18B HUMAN STANDARD; P
095998; 096027; 095993; Q9UBR7;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                              InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; Lipcoln cytFABP.
Pfam; PF00061; Lipcoln 1.
PRINTS; PR00178; FATTYACIBP.
PROSITE; PS00214; FABP; 1.
                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95034308; PubMed=7947321;
Ho L., Mercola M., Gudas L.J.;
"Xenopus laevis cellular retinoic
spatial expression pattern during
Mech. Dev. 47:53-64(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                   SEQUENCE
                                                                                                                                                                              Vitamin A;
INIT MET
                                                                                                                                                                                                                                                       EMBL; S74933; AAB32580.1;
HSSP; P29373; 1CBS.
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retinoic acid-binding protein, cellular Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CYTOSOLIC CRABPS MAY REGULATE THE ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS. SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAB
                                                                                                                                                                                                                                                                                                                                                                                  TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKMKPRRNLEE 11
                                                                                            WKMKPRRNLEE
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                                                                           WKMKQSENFEE
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                                                                                                                                                                 137
                                                                                                                                                                                      Transport.
                                                                                                                      Conservative
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                                                                                                                                                                  15524 MW;
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                                                                                                                 Score 40; UB J
Pred. No. 7.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No.
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                                                                                                                                                                  2193DDE7B095EC4A CRC64;
                                                                                                                                                                              SIMILARITY
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early embryogenesis.";
                                                                                                                                40; DB 1
No. 7.3;
                      197
                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                                                           Length 137;
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Aizawa Y.,
Ushio S., N
CARBOHYD
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DISULFID
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                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
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15-JUN-2002 (Rel. 41, I
Interleukin-18 binding
                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poxvirus.";
Virology 257:297-302(1999).
-!- FUNCTION: Binds to IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A), SI 55-58; 61-72; 89-93; 105-142 AND 1 MEDLINE=99192308; PubMed=10094485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novick D., Kim
Rubinstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 29
AND TISSUE SPECIFICITY.
MEDLINE=99146382; PubMed=10023777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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"Identification of human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Interleukin-18 binding
                                                                                                                                                                                                       Pfam; PF00047;
                                                                                                                                                                                  mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 3 ISOFORMS; A/IL-18BPA, B/IL-18BPB 18BPC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING TISSUE SPECIFICITY: Strongly expressed in heart, lung, p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Binds to IL-18 and inhibits its activity. an inhibitor of the early TH1 cytokine response. SUBCELLULAR LOCATION: Secreted (Potential). ALITERNATIVE PRODUCTS: 3 ISOFORMS; A/IL-18BPA, B/IL-
                                                                                                                                                                                                                                                                               AF110798; AAD17187.1;
AF110798; AAD17188.1;
AF110798; AAD17189.1;
AF110799; AAD17190.1;
AF110800; AAD17190.1;
AF110801; AAD17191.1;
AF110801; AAD177192.1;
AB1019504; BAA76374.1;
AF122906; AAD41051.1;
AF122906; AAD41051.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
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SIMILARITY:
                                                                                                                                                                                                                                               604113;
                                                                                                                                                                                                                                                                HGNC:5987; IL18BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akita K., Taniai M., Torigoe K., Nukada Y., Tanimoto T., Ikegami and expression of interleukin-18 t. 445:338-342(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10:127-136(1999)
                                                                                                                                                                                                                        IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update) protein precursor (IL-
                                                                                                                                                                                Glycoprotein; Signal; Alternative splicing
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                INTERLEUKIN-18 BINDING P
IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
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N-LINKED (GLCNAC...) (
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Torigoe K., T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, ALTERNATIVE
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AND TISSUE SPECIFICITY
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SEQUENCE
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029368;
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McKell L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J., Weidman K.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Arginyl-tRNA synthetase (EC 6.1.1.19) (Argians or AF0894)
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                        TIGREAM8; TIGRO0456; argS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
Aminoacyl-trna synthetase; Protein biosynthesis;
                                                                           InterPro; IPR001412; tRNA-synt I.
Pfam; PF00750; tRNA-synt Id; 1.
Pfam; PF03405; N-Arg; 1.
PRINTS; PR01038; TRNASYNTHARG.
                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                      diphosphate + L-arginyl-trna(Arg).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390.364-370(1997).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
                                                                                                                                                                                                 EMBL; AE001042; AAB90346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgidus.
                                                                                                                                                                                   TIGR; AF0894;
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                                                                                                                                                                 InterPro;
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IPR005148;
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Pred. No. 11;
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SEQUENCE
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a putative polyamine transporter.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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PFOSITE; PS00218; AMINO_ACID_PERMEASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF080132; AAC31569.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative polyamine transporter.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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IPR004841; Permease.
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Search completed: March 26, Job time : 5.36047 secs

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168.726 Million cell update
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             hypothetical prote immediate-early pr retinoic acid-bind xCRABP - African c hypothetical prote hypothetical prote
                                                                                                                                                        hypothetical prote hypothetical prote probable heat shoc bacteriophage prot hypothetical prote hypothetical prote dihydrolipoamide S
                                                                                             hypothetical prote
ABC-type transport
hypothetical prote
NADH oxidase-relat
                                                                                                                                         hypothetical prote alpha-glucuronidas
                                                                                                                                                                                                                                         conserved hypothet ribonuclease III (
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                                                                                                                                 glutamate synthase
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                                                                   transcription fact
probable heat shoc
                                                                                     hypothetical prote
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prote
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ALIGNMENTS

A; Molecule type: protein
A; Residues: 1-6 <2R2>
A; Residues: 1-6 <2R2>
R; Fulda, M.; Heinz, E.; Wolter, F.P.
R; Fulda, M.; Heinz, E.; Wolter, F.P.
Mol. Gen. Genet. 242, 241-249, 1994
A; Title: The fadD gene of Escherichia coli
A; Reference number: S41588; MUID:94150456;
A; Accession: S41590 R;Barrell, B.G.; Rajandream, M.A.; McDougall, R.C.; submitted to the EMBL Data Library, November 1999 A;Reference number: Z25045 A;Accession: T50202 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA RESULT 1 T50202 N;Alternate names: ribonuclease D C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002 C;Accession: S01223; A30431; S41590; D64941; S42849; D21915 R;Zhang, J.; Deutscher, M.P. conserved hypothetical protein SPAC25B8.15c [imported] - fission yeast (Schizosaccharomy(C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 C;Accession: T50202 R; Zhang, J.; Deutscher, M.P.
Nucleic Acids Res. 16, 6265-6278, 1988
A;Title: Escherichia coli RNase D: sequencing of the rnd structural gene and purification A;Reference number: S01223; MUID:88289400; PMID:3041371
A;Accession: S01223 片 Ş A;Gene: SPDB:SPAC25B8.15c A;Map position: 1 A; Cross-references: EMBL: AL13: A; Experimental source: strain A; Molecule type: DNA A;Cross-references: EMBL:X07055; NID:g42770; PIDN:CAA30098.1; PID:g581215 A;Accession: A30431 A; Molecule type: DNA A; Residues: 1-375 < ZHA> ribonuclease III (EC 3.1.26.3) rnd - Escherichia coli (strain K-12) A;Residues: 1-237 <BAR> Query Match Best Local Matches 220 RMKPRRKLRNMDDYL 234 2 KMKPRRNLEE-DDYL 15 l Similarity 10; Conservat Conservative EMBL:AL133225; PIDN:CAB61781.1; ce: strain 972h(-); cosmid c25B8 52.9%; Score 45.5; Di Pred. No. 4.3; 1; Mismatches K12 is located PMID:8107670 BB 2 McLean, GSPDB:GN00066; SPDB:SPAC25B8.15c Length 237; Indels close to 1; rnd Gaps at 39.6 ŗ min õ

t he

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A;Cross-references: GB:X70994; NID:g433478; PIDN:CAA50322.1; PID:g581071
A;Experimental source: strain K12
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64941
RNase D, pro
C;Species:
                                                                                                                                                                                                                                                                                                                                                            A; October type: DNA
A; Molecule type: DNA
A; Residues: 1-375 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB35936.1; PID:g13361980; GSPDB:GN00154
A; Cross-references: strain O157:H7, substrain RIMD 0509952
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A;Start codon: TTG
C;Superfamily: ribonuclease D
C;Keywords: exonuclease; hydrolase
C;Keywords: exonuclease; hydrolase
F;1-375/Product: ribonuclease D #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A99943
C;Accession: A99943
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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A;Molecule type: DNA
A;Residues: 1-375 <BLAT>
A;Cross-references: GB:AE000274; GB:U00096; NID:g1788089; PIDN:AAC74874.1; PID:g1788105;
A;Experimental source: strain K-12, substrain MG1655
                                             RESULT 4
E85791
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNase D, processes tRNA precursor [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                                                                           Superfamily: ribonuclease
                                                                                                                                                                                                                                                                                                                                                        ;Gene: EC02513
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;Residues: 'L',2-38 <FU2>
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                             342
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nes 7; Conserv
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  processes tRNA precursor [imported] - Escherichia coli (strain 0157:H7,
s: Escherichia coli
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Pred. No. 8.5;
2; Mismatches
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Pred. No. 8.5;
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  hypothetical protein C01F1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note type: DNA
A; Molecule type: DNA
A; Residues: 1-532 < ROU's
A; Cross-references: EMBL: AC004684; NID: g3236234; PID: g3236255
A; Cross-references: cultivar Columbia
The Benito, M.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2g37730 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F13M2.23 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02539; D84796
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C;Superfamily: ribonuclease D
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A;Cross-references: GB:AE005174; NID:g12515844; PIDN:AAG56793.1; GSPDB:GN00145; UWGP:Z284
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A;Introns: 165/2; 295/3; 478/3
C;Superfamily: Arabidopsis hypothetical protein F13M22.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84796
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A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A;Reference number: Z14677
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A;Map position: 2
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A;Residues: 1-532 <STO>
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                                                                                                                              Query Match
Best Local
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476
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                                                                                                                              Local Similarity
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                                               1 WKMKPRR-----NLEED 12
WKMAPRROCCEIVNSEED 493
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7; Conserv
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Pred. No.
                                                                                                                              Score 44;
Pred. No.
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3.5;
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L.; Tallon, L.
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH1754
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable heat shock transcription factor - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39150 C;Accession: T39150 R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
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A;Molecule type: DNA
A;Mesidues: 1-312 < JOH>
A;Cross-references: EMBL:U58761; NID:g1330391; PID:g1330396; PIDN:AAB00716.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone CO1F1
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A;Map position: 1
A;Introns: 10/3; 40/3;
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A;Cross-references: EMBL:299168; PIDN:CAB16301.1; GSPDB:GN00066; SPDB:SPAC8C9.14
A;Experimental source: strain 972h-; cosmid c8C9
C;Genetics:
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A;Accession: T39150
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Map position: 2
A;Introns: 36/2; 271/1
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A; Status: preliminary
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bacteriophage protein homolog lin2581 [imported] - Listeria innocua (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introns: 10/3; 40/3; 67/2; 86/3
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Pred. No.
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Pred. No.
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Kowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: D96692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T49020
R;Purnelle, B.; Masuy, D.; Goffeau, A.; Boutry, M.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 2000
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Best Local Similarity
Thes 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T12I7.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F3C22.70 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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A;Experimental source: strain Clip11262
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A;Experimental source: cultivar Columbia; BAC clone F3C22
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A;Accession: T49020
                                                                                                                      A;Gene: T12I7.9
                                                                                                                                                                    A;Cross-references:
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                                              Query Match
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Local Similarity 50.
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  ; Score 42; DB
; Pred. No. 31;
3; Mismatches
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                                                                                                                                                                    NID:g11054573;
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Pred. No.
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9.6;
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A;Cross-references: GB:M57435; GB:M31542; NID:g143375; PIDN:AAA62683.1; PID:g143379
R;Kinst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; CR.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumamoto, H.; Yanano, K.; Yata, K.; Yoshida, K.
A, Yitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A, Reference number: A69580; MUID:38044033; PMID:3384377
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C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 20-Jun-2000
C;Accession: D36718; B69674
R;Hemilae, H.; Palva, A.; Paulin, L.; Arvidson, S.; Palva, I.
J. Bacteriol. 172, 5052-5063, 1990
A;Title: Secretory S complex of Bacillus subtilis: sequence analysis and identity to pyr A;Reference number: A36718; MUID:90368558; PMID:1697575
                                                                                                                     submitted to the Protein Sequence Database, A;Reference number: Z25013
A;Accession: T49021
                                                                                                                                                                                                                C;Accession: T49021
R;Purnelle, B.; Masuy, D.; Goffeau,
                                                                                                                                                                                                                                                                       hypothetical protein F3C22.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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A; Residues: 1-442 < HEM>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <PUR>
A;Cross-references: EMB
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A;Experimental source: strain:
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A;Status: preliminary; nucleic acid sequence not shown; translation
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   EMBL:AL353912;
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Pred. No. 33;
3; Mismatches
   GSPDB:GN00061; ATSP:F3C22.80
                                                                                                                                                                                      A.; Boutry, M.; Mewes, H.W.; Rudd, atabase, April 2000
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alpha-glucuronidase (EC 3.2.1.-) precursor - fungus (Trichoderma reesei)
N,Alternate names: GLRI
C;Species: Trichoderma reesei
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 17-Mar-1999
C;Accession: JC4836
R,Margolles-Clark, E.; Saloheimo, M.; Siika-aho, M.; Penttilae, M.
Gene 172, 171-172, 1996
A;Title: The alpha-glucuronidase-encoding gene of Trichoderma reesei.
A;Recession: JC4836
A;Recession: JC4836
A;Molecule type: mRNA
A;Recession: JC4837
ANROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: cultivar Columbia;
C;Genetics:
A;Gene: ATSP:F3C22.80
A;Map position: 3
A;Introns: 4/2; 294/3; 339/3
                                                                                                                                                                                                                                                                                                                                                                                 glutamate synthase large subunit gltB [imported] - Agrobacterium tumefaciens (;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: ACLS94
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:268706; NID:gl419337; PID:e218512; PID:gl419338 C;Comment: This enzyme releases glucuronic acid attached to xylose units C;Genetics:
A;Gene: glr1
C;Keywords: glycosidase; hydrolase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-847/Product: alpha-glucuronidase #status predicted <MAT>
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Best Local Similarity
""" hes 6; Conserv:
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1832 < CUI>
A; Cross-references: GB: AE008688;
A; Experimental source: strain C5:
C; Genetics:
                                                                                                                                                                                                                                              A;Title: The Genome of the Natural Genetic Engineer A;Reference number: AB2577; PMID:11743193 A;Accession: AC2594
                                                                                                                                                                                                                                                                                                         ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
                                                                                                                                                                                                                          A;Status: preliminary
                   Query Match
Best Local S
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Best Local
                                                                                position: circular chromosome
                                                                                                   gltB
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53.8%;
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42.9%;
                   48.8%;
                                                                                                                                              C58
Score 42; DB:
Pred. No. 1.4e
3; Mismatches
                                                                                                                                                                 PIDN: AAL41169.1;
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Pred. No.
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Pred. No.
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33;
                                          DB 2;
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                                                                                                                                                                 PID:g17738468; GSPDB:GN00186
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                                          Length 1832;
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Conservative

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0

Gaps

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RESULT 15
D97376
D97376
hypothetical protein AGR_C_235 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Aace: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Aacession: D97376
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Accession: D97376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1858 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK85965.1; PID:g15155024; GSPDB:GN00169
C;Genetics:
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Search completed: March 26, 2003, 16:50:36 Job time : 12.5465 secs
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A;Map position: circular chromosome
                                                                                                                                                                                                                                    Query Match 48.8%; Score 42; DB 2; Length 1858; Best Local Similarity 53.8%; Pred. No. 1.5e+02; Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                                                3 MKPRRNLEEDDYL 15
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382 LRPLRTVETDDYL 394
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356 LRPLRTVETDDYL 368
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Maximum DB
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
  Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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9 US-10-010-667A-21

10 US-09-747-835A-50

10 US-09-747-835A-51

9 US-10-012-896-879

9 US-09-895-733-879

9 US-09-895-814-879

9 US-09-895-814-879

10 US-10-011-095-2

10 US-10-010-667A-2

10 US-09-759-113-879

10 US-09-759-113-879

10 US-09-815-242-879

10 US-09-815-242-879

10 US-09-815-242-12629

10 US-09-815-242-12629

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10 US-09-815-242-12629
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          Sequence 21, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 819, Appl Sequence 879, Appl Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 879, App Sequence 39, Appli Sequence 39, Appli Sequence 342, Appli Sequence 5422, App
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	42	42	42	42	42	42	42	43	43
44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1		45.2		45.2		45.2	45.2			46.2
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e 12,	17,	Sequence 46, Appl	•	46,	46,	67	•	25,	22,	21,	Sequence 72, Appl	70,		ü	8,	73	2	Sequence 2, Appli	Sequence 4, Appli	21, /	Sequence 71, Appl	68,	e 26,	Sequence 102, App	Sequence 61, Appl

ALIGNMENTS

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Sequence 21, Application US/10011095
Publication No. US20030045682A1
Publication No. US20030045682A1
PublicaNT Northarion
APPLICANT Hubert, Rene S.
APPLICANT Hubert, Rene S.
APPLICANT Raitano, Arthur B.
APPLICANT Saffran, Douglas C.
APPLICANT Saffran, Douglas C.
APPLICANT Saffran, Douglas C.
APPLICANT NUTHODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 51152001610
CURRENT FILING DATE: 1998-06-01
FILE REPLICANTON NUMBER: 09/323,873
PRIOR PILING DATE: 1999-06-01
PRIOR APPLICANTON NUMBER: 09/023,873
PRIOR PILING DATE: 1999-06-01
PRIOR APPLICANTON NUMBER: 09/031,183
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICANTON NUMBER: 09/091,183
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICANTON NUMBER: 09/091,183
PRIOR FILING DATE: 1998-06-30

UMMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
CORRENTE INFORMATION: STEAP-1 PEPTIDE
US-10-011-095-21

Ouery Match
Best Local Similarity 100.0%; Score 93; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
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Matches 15; Conservative 0; Mismatches 0; Indels No. 4.5e-08;
Matches 16; Mismatches 16; Mismatches
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APPLICANT: Raitan, Douglas C.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTWARE: PASUSEQ for Windows Version 4.0
ISEQ ID NO 21
LENGTH: 15
TYPE: PRT
                                                                               APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
ITLE OF INVENTION: METRIODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
ITILE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/52,317
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/552,317
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
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Matches
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Best Local Similarity
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APPLICANT: Huber
APPLICANT: Leone
                               NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version
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ID NO 50
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US20020146692A1
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Leong, Kahan
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100.0%; Pred. No. 4.5e-08;
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APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
ITILE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/520,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-20
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
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Best Local Similarity
Matches 15; Conserve
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US-09-747-835A-50
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                                                                                                                                                                                         US-10-012-896-879
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PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOPTWARE: PatentIn version 3.0
SEQ ID NO 51
LENGTH: 267
                                                                                                                        Sequence 879, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT:
APPLICANT:
APPLICANT:
                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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TYPE: PRT
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Liu, Chenghua
                                         Harlocker, Susan L.
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Wang, Dunrui
  Jiang, Yuqiu
Kalos, Michael D
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Pred. No. 8.2e-07;
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Pred. No. 8.2e-07;
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Retter, Marc W. Stolk,

John

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CURRENT APPLICATION NUMBER: US/09/802,520
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: CMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US$/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEO ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENCTH: 339
                                                                                                                                      JS-09-802-520-11
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09802520 Publication No. US20020187472A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserva
                                                                   Matches
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lal, Preeti
APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Craig H.
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                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STEAP-RELATED PROTEIN FILE REFERENCE: PC-0037 US
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ORGANISM: Homo sapiens
                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
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 277 WIDIKQFVWYTPPTF 291
                 1 WIDIKQFVWYTPPTF 15
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Carter, Darrick
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                                                                   Conservative
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                                                                                   100.0%;
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100.0%; Pred. No. 1e-06;
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                                                                 Score 93; DB 9;
Pred. No. 1e-06;
; Mismatches
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                                                                                                 DB 9; Length 339;
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US-09-895-814-879
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                                                                                                                                                                                                                                                                                                           Sequence 879, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FANGER, GARY R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                 APPLICANT:
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           PPLICANT
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Dillon, Davin C.
Mitcham, Jennifer L.
Hural, John
McNeill, Patricia D.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
                                                                                                                   Vedvick, Thomas
Carter, Darrick
Li, Samuel X.
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Kalos, Michael D.
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Mitcham, Jennifer L.
Harlocker, Susan L.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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                                                                  Skeiky, Yasir A.W.
Hepler, William T.
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Carter, Darrick
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                                                        Henderson, Robert A.
                                                                                                      Wang, Aijun
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                                                                                       Yasir A.W.
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Pred. No. 1e-
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 60/87,520
PRIOR APPLICATION NUMBER: 60/87,520
PRIOR APPLICATION NUMBER: 60/87,520
PRIOR APPLICATION NUMBER: 60/91,183
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/91,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 339
TYPE: PRI
COCANTAN. Artificial Socience
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210111.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-814-879
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Sequence 2, Application US/1001067A
publication No. US20030055217A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10011095
Publication No. US20030045682A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                  277
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APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 51158201601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/081,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PAT
; ORGANISM: Homo sapiens
US-10-010-667A-2
                                 Query Match
Best Local Similarity
Watches 15; Conserve
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                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASUSEQ for Windows Version 3.(
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILS REFERENCE: 210121.427C23
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1 WIDIKQFVWYTPPTF 15
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Dillon, Davin C.
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Vedvick, Thomas S.
Carter, Darrick
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ilarity 100.0%;
Conservative 0
                                                    100.0%; Score 93; DB 10 ilarity 100.0%; Pred. No. 1e-06; Conservative 0; Mismatches
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Pred. No. 1e-06;
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RESULT 12 US-09-780-669-879

Sequence 879, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION:

Xu, Jiangchun Dillon, Davin C. Mitcham, Jennifer L.

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Sequence 879, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEO ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 879

LENGTH: 339

TYPE: PRT
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US-09-822-827-879
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                                                                                                     ; ORGANISM: Homo sapiens
US-09-822-827-879
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIACHOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
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                                Local Similarity
les 15; Conserv
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Local Similarity 100.0%;
Les 15; Conservative (
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1 WIDIKQFVWYTPPTF 15
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Hepler, William
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Carter, Darrick
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Pred. No. le-
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Pred. No.
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RESULT 14
US-09-854-816-39
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Best Local Similarity 60.0
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                                                                                                                       Sequence 33, Application US/09854816 Patent No. US20020151473A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 39:
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timoth
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
James A. Wells TITLE OF INVENTION: Constrained Helical Peptides and Methods of
                                                                                                          APPLICANT: Andrew C. Braisted
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/965,056 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 268 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09854816
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                                               J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
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J. Christopher Phelan
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                                 Melissa A. Starovasnik
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NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSE: Geneentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER RAPADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 40thnown>
PRIOR APPLICATION NUMBER: 08/965,056
FILING DATE: 40thnown>
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, PhD., Timothy E.
RECISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 91005R2
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
TELEPHONE: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-854-816-33

48.44; Score 45; DB 10; 1
Search completed: March 26, 2003, 17:04:17 Job time: 11:1163 secs
                                                                                                                                                                                        Query Match 48.4%; Score 45; DB 10; Length 269; Best Local Similarity 60.0%; Pred. No. 15; Matches 6; Conservative 2; Mismatches 2; Indels
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

6: /cgn2_6/ptodata/1
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Match Length DB
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46.007 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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       GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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    US-09-323-873A-21
US-09-323-873A-2
US-08-965-056-39
US-08-965-056-39
US-08-118-270-45
PCT-US39-08528-45
US-07-956-483-13
US-08-817-441-47
US-08-817-441-102
US-08-965-056-68
US-08-965-056-68
US-08-965-056-69
US-08-965-056-81
US-08-965-056-81
US-08-965-056-81
US-08-965-056-81
US-08-965-056-14
US-08-965-056-72
US-08-965-056-21
US-08-965-056-22
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Sequence 21, Appl
Sequence 2, Appli
Sequence 39, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 47, Appl
Sequence 83, Appl
Sequence 61, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 72, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 25, Appl
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43.0	43.5	43.5	43.5	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1
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US-09-433-428D-67	US-08-976-255-11	US-09-083-521-7	US-08-976-255-10	US-08-976-255-14	US-08-647-714-6	US-08-388-809-6	US-08-022-835-6	US-09-492-739-28	US-09-134-075-28	US-08-448-603A-28	US-09-257-490-15	US-09-109-916-46	US-08-468-059-46	US-08-471-770-46	US-08-470-202-46	US-08-965-056-67	US-08-965-056-37
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
67,	11,	7,	10,	14,	,	٠,	6,	28,	28,	28,	15,	46,	46	46,	46,	67,	37,
App1	App	Appli	Appl	Appl	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl

ALIGNMENTS

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Sequence 2, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOI
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 199-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-10
APRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: STEAP-1 PEPTIDE
US-09-323-873A-21
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US-09-323-873A-21
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US-09-323-873A-2
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mes 15; Conserv
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1 WIDIKQFVWYTPPTF 15
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100.0%; Pred. No. 2.4e-08;
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FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
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US-09-323-873A-2
                                                                                      US-08-965-056-39
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  Matches
                     Query Match
Best Local Similarity
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Patent No. 6271198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOYCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb I
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Constrained TITLE OF INVENTION: Making Same NUMBER OF SEQUENCES: 113
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                                                                                                                      LENGTH: 268 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/965,056 FILING DATE: 05-No. 6271198-1997
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                                                                                                       TOPOLOGY:
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1 DNA Way
  48.4%;
milarity 60.0%;
Conservative
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James A. Wells
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Melissa A. Starovasnik
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Robert S. McDowell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.44 Mb floppy disk
Score 45; DB 4; Length 268; Pred. No. 11; 2; Mismatches 2; Indels
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US-08-965-056+33
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Best Local S
Matches 6
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674
                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb fle
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
                                                            APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: RECEPTORS, AND C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                               203 WEDITQWLWY 212
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 269 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                            Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                              1 WIDIKQFVWY 10
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                                                                                                                                                              Application US/08118270
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419 Seventh Street, N.W.,
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Robert S. McDowell
J. Christopher Phelan
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                             Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                G-COUPLED PROTEIN
COMPOSITIONS AND METHODS THEREOF
   Suite 300
                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                            Length 269
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                                                                                                                                                             ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-193

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION TO NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: TOWNERS TO THE TOWNERS TO THE TOWNERS TOW
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GENERAL INFORMATION:
APPLICANT: New York University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 248633
TELEPHONE: 202-628-5197
                                                                 NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 48.4%;
Local Similarity 33.3%;
les 5; Conservative
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 WVELYNFIWHHPWAF 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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Y: USA
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linear
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Pred. No. 15;
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US-07-956-483-13
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                                                                                     US-07-956-483-13
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                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             TELEPAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: KIENY, Marie-Paule
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 9
PILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-NOV-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. BOX
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 WVELYNFIWHHPWAF 70
                                                                                                          STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 22313-1404
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Local Similarity 33.3%;
les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                    LENGTH:
                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
1 WIDIKOFVWY 10
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                                                                                                                                      i: 865 amino acids amino acid
                                                                                                                                                                                                                                                                  Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virgini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                         (703) 836-6620
                                                                                                                                                                                                                                                                                          TUMBER: FR 91 05392
02-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                               DNA (genomic)
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                                        48.4%;
60.0%;
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                              Mismatches
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Pred. No.
                                         Score 45;
Pred. No.
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                                        DB
36;
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                                                        Length 865
                              Indels
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US-08-472-240A-4
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                                                                                                                                                                                                                                             US-08-887-534A-83
                                                                                                                                                                                  Sequence 83, Application US/08887534A Patent No. 6455323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.4%;
Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      Matchee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/472,240A
EILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,483
PILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENERAL INFORMATION: APPLICANT: KIENY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 887 amino acids
                                                                     NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PATENTIA RE-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                APPLICANT: Holden, David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL HYBRID, TITLE OF INVENTION: 9p160 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                           703 WEDITQWLWY 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 22313-1404
               STATE: Illinois
COUNTRY: United States
                                                     CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L
REGISTRATION NUMBER: :
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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1..854
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                                                                                                                                                  ANTI-BACTERIAL METHODS AND MATERIALS
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                 of America
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Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47,
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                                           APPLICATION NUMBER: US/08/
FILING DATE: 11-UL-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/FR
PILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
                                                                                                                                                 ZIP: 2005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,534A
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                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR TITLE OF INVENTION: SUBTYPE) ANTIGENS NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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Local Similarity 58.3%;
les 7; Conservative
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ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-0448
TELEFAX: (312) 474-6600
              APPLICATION NUMBER: FR 9. FILING DATE: 20-OCT-1994
                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DIKQFVWYTPPT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 403 amino acids
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                                                                                                                                                                                                                                                                              USA
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BORMAN, ANDREW
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DONJON DE SAINT-MARTIN, JACQELINE
COHEN, JAQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUETARD, DENISE
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                                FR 9412554
                                                                                                                                        US/08/817,441
                                                                                 PCT/FR 95/01391
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Pred. No.
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RESULT 11
US-08-912-129A-61
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Patent No. 5922533
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
TYPE: amino acid
                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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(NPORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                  TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 WEDITKWLWY 169
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Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Abbott
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road
                                                                                                                                                                                                    FILING DATE:
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amino acid
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                                                                                    847-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HACKETT
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                                                                                                                                                                                                                                                                    15-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ALAN M
                                                                                                                                                                                                                                                                                                                   MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , JOHN JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATHERINE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELIZABETH A.
                                                                                                                                                                                                                                                                                     US/08/912,129A
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                                                                                                                                                                                                                                                                                                                   (Windows 95)
(ASCII format output)
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Pred. No.
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21
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-912-129A-61
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                                             ; MOLECULE TYPE: US-08-817-441-102
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Best Local Similarity 50.0
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Patent No.
Query Match
Best Local Similarity
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                                                                                                                                   TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/FR
FILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 941
FILING DATB: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: FR 950
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3315
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                                                                                                                      ENGTH:
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5. 6399294
                                                                                                         amino acid
                                                                                                                   877 amino acids
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GUETARD, DENISE
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BORMAN, ANDREW
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DONJON DE SAINT-MARTIN, JACQELINE
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                                                                              linear
                                                            protein
                                                                                           single
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46.2%;
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Score 43;
Pred. No.
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                                                                                       Patent No. 6271198
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andrew C
APPLICANT: J. Kevii
APPLICANT: Robert S
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Patent No. 6271198
                                                                                                                                                                 Sequence 68, Application US/08965056 Patent No. 6271198
                                                                                                                                                                                                                                                                                                                                           Matches
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Melissa A. Starovasni
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained
TITLE OF INVENTION: Making Same
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
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ZIP: 94080
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les 5; Conserv
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CITY: South San Francisco
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                       INVENTION:
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                                                                     J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
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J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
                                        James A. Wells
                                                        Melissa A. Starovasnik
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Constrained Helical Peptides and Methods of Making Same
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Pred. No. 32;
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US-08-965-056-71
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Patent No. 6
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FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOYCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
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INFORMATION FOR SEQ ID NO: 68:
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APPLICANT:
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LENGTH: 268 amino acids
TYPE: Amino Acid
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Local Similarity 50.0%;
nes 5; Conservative
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STREET: 1 DNA Way
CITY: South San Francisco
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Melissa A. Starovasnik
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Robert S. McDowell
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Pred. No.
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Length 268;

°. Gaps

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REPERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION IMFORMATION:
TELECHOME: 650/225-8674
TELECHOME: 650/225-8674
TELECHOME: 650/225-8674
TELECHOME: 268 anino acide
TOPOLOGY: Linear
US-08-965-056-71

Query Match
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0

Oy 1 MIDIKOFWRY 10
Db 202 MFDISRMIMY 211

Search completed: March 26, 2003, 16:51:41

Job time: 10.593 secs
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Minimum DB :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
    March 26, 2003, 16:43:45; Search time 15.6977 Seconds (without alignments) 196.889 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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93
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sp_invertebrate:*
sp_mammal:*
sp_mac:*
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sp_phage:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_virus:*
sp_vriclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Q90dn6 human immun	Q9ill6 human immun	Q9qiu8 human immun	Q9qiw7 human immun	Q9yxq1 human immun	Q9yxr4 human immun	Q9evq0 escherichia	Q97002 human immun	Q9ijl9 human immun	Q8uht8 agrobacteri	Q98ck3 rhizobium l	Q924j9 mus musculu	Q924z2 mus musculu	Q9cwr7 mus musculu	Q9g150 sus scrofa	Description

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15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
012005	Q8Q2X5	012007	012010	012004	Q9E1S7	Q72940	012002	Q87628	Q902H5	012008	092762	Q8UL54	Q8UL55	056567	041641	Q70003	056113	089292	Q9IV31	Q8Q2X4	Q9QKH9	Q9QKI3	Q9QKI4	Q8Q2X3	Q78120	Q90E72	Q8UQY9
012005	Q8q2x5	012007	012010	012004	Q9e1s7	Q72940	012002	Q87628	Q902h5	012008	092762	Q8u154	Q8u155	056567	041641	Q70003	056113	089292	Q91v31	Q8q2x4	Q9qkh9	Q9qki3	Q9qki4	Q8q2x3	Q78120	Q90e72	Q8uqy9
chimpanzee	human immun	chimpanzee	chimpanzee	chimpanzee	human immun	human immun	D)	chimpanzee	human immun	chimpanzee	human immun	human immun	human immun	human immun	human immun	human immun	human immun	human immun	human immun	human immun	human immun						

ALIGNMENTS

RESULT 2 Q9CWR7 ID Q9CWR7, PRELIMINARY; PRT; 339 AA. AC Q9CWR7, PRELIMINARY; PRT; 339 AA. DT 01-JUN-2001 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)	Q9GL50 ID Q9GL50 PRELIMINARY; PRT; 338 AA. AC Q9GL50; DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DE Six transmembrane endothelial antigen of PAEC. OS Sus secrofa (Pig). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus. OX NCEI_TaxID=9823; RN [1] RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Heslan JM., Soulillou JP., Charreau B.; RT "Differential gene expression in endothelial cells during TNF-alpha- RT and IngS-mediated activation."; RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. DR EMBL, AF319659; AAG33868.1; KW Transmembrane. SQ SEQUENCE 338 AA; 39918 MW; ED490E86E067A32B CRC64; Guery Match Best Local Similarity 86.7%; Pred. No. 3.4e-07; Matches 13; Conservative 2; Mismatches 0; Gaps OY 1 WIDIKQFVWYTPPTF 15 Db 276 WVDIKQFVWYTPPTF 290	
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Q924ZZ

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AC Q924

AC Q924

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DT 01-J

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
A Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsub Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bonaldo M.F.,
A Susuki H., Sato K., Bonaldo M.F.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,
A Wunchay M., Andri R., Waltz C., Whittaker C., Wilming L.,
A Wunchay M., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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Q924Z2;
Q1-DEC-2001
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                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL, AY029584; AAK50537.1; -
MGD, MGI:1915678; 1010001DO1Rik.
SEQUENCE 339 AA; 39109 MW; 32A2C29F2E333BI
                                                                                                                                                                                                                                                                                    "Prostate and non-prostate expression of human STEAP.";
                                                                                                                                                                                                                                                                                                                                                   Serru V.,
Loric S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AKO10437; BABZ6938.1; -.
MGD; MGI:1917608; Steap.
SEQUENCE 339 AA; 39264 MW;
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STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
MEDLINE=21085660; PubMed=11217881;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Serru V., Manivet P.,
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Mammalia; Eutheria;
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STEAP OR 2410007B19RIK.
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  1 WIDIKOFVWYTPPTF
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Rodentia;
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                                                                                      Score 80; DB 11;
Pred. No. 2.4e-05;
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Pred. No. 2.4e-05
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01-OCT-2001
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01-JUN-2002
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Q924J9;
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"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
"Murine six-transmembrane epithelial antigen of the prostate, prostate stem cell antigen, and prostate-specific membrane antigen: prostate-specific cell-surface antigens highly expressed in prostate cancer of transgenic adenocations mouse prostate mice.";
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Six-transmembrane epithelial antigen of the prostate
                                                                                                      SEQUENCE 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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EMBL; AF297098; AAK83126.1; -.
MGD; MGI:1917608; Steap.
                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                         DNA Res.
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Mammalia; Eutheria; Rodentia;
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Pro; IPR000567; SBP_bac_1.
PF01547; SBP_bacterial_1; 1.
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53.8%;
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Pred. No.
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Pred. No.
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2;
       DB 16;
4.9;
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                                   Length 448;
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Q9IJL9;
01-OCT-2000
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MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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OBUHT8;
O1-JUN-2002 (TrEMBLrel. 21,
O1-JUN-2002 (TrEMBLrel. 21,
O1-JUN-2002 (TrEMBLrel. 21,
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Egp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
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AGLE OR ATU0591 OR AGR C 1045.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                ENV
                                                                                                             Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
                                    duman immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169
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SEQUENCE
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"Evidence for a high frequency of HIV-1 subtype F info heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
EMBL; AF220713; AAF76832.1; -.
InterPro; IPR000328; Env GP41.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw
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                                                                                                                                                                                                              AIDS; C
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                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                        Allen E.E.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=HIVBR020.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. WHO and NIAID Networks for HIV Isolation and Characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hahn B.H.;
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WFDISQWLWY 669
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6; Conserv
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122 AA;
                                                                                                                                                                                     844 AA;
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                                                                                                                                                                                     95594 MW;
                                                                                                              49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.5%;
                                                                                                                                                                                                                                                                                                                                 _GP41.
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Pred. No. 3.9;
2; Mismatches
                                                                                          Score 46; DB Pred. No. 30; 2; Mismatches
                                                                                          2
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                                                                                                                                                                                        0E02E379CFD17691
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                                                                                                                                         Length 844;
                                                                                                                                                                                        CRC64;
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                                                                                             Indels
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RESULT 10
Q9YXR
ID Q9YXR
AC Q9YXR
AC Q9YXR
AC Q9YXR
DT 01-MA
DT 01-DE
Envel
GN ENV.
OS Human
OC Virus
OC NCBI.
RN [1]
RC STRAI
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Q9EVQ0
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Best Local S
Matches 7
                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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Q9EVQ0;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YXR4 PRELIMINARY; PRT; 12 AA.
Q9YXR4;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 12,2 kDa protein.
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF034039; AAC79291.1; -. InterPro; IPR000328; Env GP41. Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanuri A., Swanson P.A.,
Costa L.J., Telles J.G.,
Rayfield M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unkmeir A., Schmidt H.;
"Structural analysis of phage-borne stx genes and their sequences in shigs toxin-producing escherichia coli and dysenteriae type 1 strains ";
Infect. Immun. 68:4856-4864(2000).
EMBL, AJ251452; CAC05542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=RJ96BRP009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 107 AA; 1
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=E32511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
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   112
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                                                                           1 WIDIKQFVWY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIDIKOFVWYTPPTF 15
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MEDITOMLMY
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7; Conserv
                                                                                                                                                                                                                                                                                                         122 122
122 AA; 14739 MW; 40D4789EB8C888C2 CRC64;
                                                                                                                                                          Conservative
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       121
                                                                                                                                                                                          48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devare S.G., Berro O.J., Savedra A., Brindeiro R., Schable C., Pieniazek
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Pred. No. 5;
2; Mismatches
                                                                                                                                                      <u>ب</u>
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                                                                                                                                                                                      Score 45; DB 15; Length 122; Pred. No. 5.7;
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                                                                                                                                                          Mismatches
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                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pieniazek D.,
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shigella
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RESULT 11

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Q9QIW7
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                                                                                                                                                                              Query Match
Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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Q9QIW7, PRELIMINARY; PRT; 122 AA.
Q9QIW7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genotyping and phenotyping analysis of B and non-B Human immunodeficiency virus type 1 subtypes from patients under HAART."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF165537; AAF08482.1; -.

Interpro; IPR000328; Env GP41.

Pfam; PF00517; GP41; 1.
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EMBL; AF034052; AAC79304.1; -.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Caride E., Hertcogs K., Larder B., I
Machado E., de Sa C.A.M., Eyer W.,
Calazans A.R., Tanuri A.;
                                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Envelope glycoprotein (Fragment).
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Costa L.J., Telles J.G.,
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STRAIN=RJ96BRP042;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane.
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    WEDITOWLWY 121
                                                                                         WIDIKQFVWY 10
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                                                                                                                                                                                                                                                                                                                                                             1
122
122 AA;
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122 AA; 14792 MW;
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                                                                                                                                                                                                                         48.48;
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Pred. No. 5.
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RESULT 13
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Q9ILL6
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Q9QIU8;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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Q9ILL6; O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NON TER
SEQUENCE
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EMBL; AF165556; AAF08501.1; -.

InterPro; IPR000328; Env_GP41.

Pfam; PF00517; GP41; 1.
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STRAIN-GP41ERRJ23;
Caride E., Hertogs K., Larder B., Dehertogh
Machado E., de Sa C.A.M., Eyer W., Passioni
Calazans A.R., Tanuri A.;
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AIDS Res. Hum. Retroviruses 16:815-819(2000).
EMBL; AF206042; AAF81998.1; -.
InterPro; IPR000338; Env GP41.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20284721; PubMed=10826488;
Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
Rayfield M.A., Sempala S.D., Lal R.B.;
"Genetic characterization and phylogenetic analysis of HIV-1 subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=UG1636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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1 WIDIKQFVWY 10
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122
122 AA;
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122 AA;
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 19, Last annotation
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                                                                         Score 45; DB 15; Length 122; Pred. No. 5.7;
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Pred. No. 5.
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L.F.C., Menezes J.A.,
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RESULT 15
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SEQUENCE
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Envelope glycoprotein (Fragment).
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Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.
"Similar distribution and continued predominance of HIV-1 subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90DN6;
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112 WFDITQWLWY 121
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112 WFDITQWLWY 121
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122 AA; 14728 MW; BEF439193281EDFE CRC64;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR '73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SUMMARIES

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probable colanic a		н	brp protein (impor	envelope protein g	hypothetical prote	probable membrane		suppressor 2 prote	maltodextrin glyco	F13K23.11 protein	protein YBR162c ho			envelope protein p	gag polyprotein -	hypothetical prote	P-loop protein - Y	regulator protein	acetyl-CoA synthet	hypothetical prote	internalin protein	hypothetical membr	acetyl-CoA synthet		envelope protein g		hypothetical prote	alpha-glucosides-b		

A;Gene: aglE A;Map position: circular chromosome

A;Cross-references: GB:AE008688; PIDN:AAL41608.1; PID:g17738945; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont)

A,Status: preliminary A;Molecule type: DNA A;Residues: 1-453 <KUR>

45	44	4 3	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
40.5	40.5	40.5	41	41	41	41	41	41	41	41	41	41	41	41	41
43.5	43.5	43.5	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44,1	44.1	44.1	44.1
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; I Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology A;Reference number: A97359; PMID:11743194
A;Accession: A97431 C;Accession: AB2649
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ester, E.W.
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB2649 alpha-glucosides-binding periplasmic protein aglE precursor [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: A97431 A; Gene: AGR C 1045 A; Map position: circular chromosome hypothetical protein aglE [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 밁 á A;Status: preliminary A;Molecule type: DNA A;Residues: 1-453 <KUR> C; Genetics: A;Cross-references: GB:AE007869; PIDN:AAK86402.1; PID:g15155534; GSPDB:GN00169 Query Match 51.6%; Best Local Similarity 53.8%; Matches 7; Conservative 169 DVKSLVWYVPENF 181 3 DIKOFVWYTPPTF 15 G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Score 48; DB: Pred. No. 4.1; 1; Mismatches , DB 4.1; 2 Length 453 Indels Agent Agrobacterium tume ٥. Gaps 0 Dupont)

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A;Molecule type: DNA
A;Residues: 1-358 <STEI>
A;Residues: 1-358 <STEI>
A;Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
A;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             envelope protein gp120/gp41 - human immunodeficiency virus type 1 (Species: human immunodeficiency virus type 1, HIV-1 A/Variety: isolate 28 (Jbate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000 (Jbate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000 (Jacession: S21998; S70425
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A;Title: Physicochemical and immunochemical characterization of A;Reference number: A23341; MUID:86242068; PMID:3718469
A;Accession: A23341
                                      RESULT
AC0065
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conserved hypothetical protein C; Species: Yersinia pestis
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A; Residues: 1-222, 'X', 224-358 <STE2>
A; Cross-references: EMBL; X61359; NID: 960182; PIDN: CAA43630.1; PID: 960183
C; Superfamily: type E retrovirus env polyprotein
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A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as A;Reference number: S21990
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A;Cross-references: GB:AE001092; GB:AE000782; NID:g2689415; PIDN:AAB91033.1; PID:g2650444
C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology
F;145-621/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson, ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997.
Nature 390, 364-370, 1997.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Wosse, C.R.; Venter, J.C.
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                                                                                                                                              R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
A;Accession: AF3544
                                                                                                                                                                                                                                                                                                                                   hypothetical membrane spanning protein BMEII0279 [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AF3544
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jan-2000
C;Accession: E65274
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A;Gene: YPO
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A;Molecule type: DNA
A;Residues: 1-331 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53521.1; PID:gl7984427; GSPDB:GN00191
A;Experimental source: strain 16M
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A; Residues: 1-662 < KLE>
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A;Accession: E69274
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-553 < KI
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Pred. No. 19;
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: AH1469
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I.D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internalin protein homolog lin0295 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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                                                                                                                                                                                                                             A;Cross-references: EMBL:Z99281; PIDN:CAB16530.1; GSPDB:GN00022; CESP:Y57G11C.31 A;Experimental source: clone Y57G11C
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                             A; Reference number:
A; Accession: T27241
                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: Z20330
                                                                                                                                                                                                                                                                                                                                                                                       R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y57G11C.31 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
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A;Experimental source: strain Clip11262
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A;Gene: BMEII0279
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                                                                                                                                                   A;Map position: 4
A;Introns: 160/3; 187/2; 309/2; 361/3
                                                                                                                                                                                         A; Gene: CESP:Y57G11C.31
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Best Local S
Matches 7
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Matches
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Local Similarity 38.5%;
nes 5; Conservative
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WPEIQOFHWPTPSLY 160
                                     WIDIKOFVWYTPPTF 15
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Pred. No. 17;
3; Mismatches
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Pred.
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Pred. No.
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No.
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13;
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Fsihi, H.
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C;Accession: S69206
R;Ballario, P.; Vittorioso, F
R;Bo J. 15, 1650-1657, 1996
A;Title: White collar-1, a ce
A; Peference number: S69206; M
A;Accession: S69206
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S69206
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89958
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A;Rolecule type: DNA
A;Residues: 1-568 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701528; PIDN:BAB42822.1; GSPDB:GN00149
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C;Accession: A89958
K;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Car submitted to the EMBL Data Library, March 1998
A;Description: Structural organization of virulence determinants in three Yersinia A;Reference number: Z18168
A;Accession: T14669
                                                                                       P-loop protein - Yersinia pestis plasmid pMT1
(;Specias: Yersinia pestis
(;Specias: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T14669
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator protein white collar 1 - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 967/3
C;Superfamily: GATA-type zinc finger homology
C;Keywords: zinc finger
C;Keywords: zinc finger
F;932-991/Domain: GATA-type zinc finger homology
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C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology
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C;Genetics:
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A; Residues: 1-1154 <BAL>
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58.3%;
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66.7%;
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06; MUID:96203083; PMID:8612589
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.5;
Pred. No. 6
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                                                                                                      Kobayashi, A.; Carrano,
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RESULT 15
S49197
                                                                                                                                                                                                                                                                                                      gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: A53034
R;Vanden Haesevelde, M; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen, J. Virol. 68, 1586-1596, 1994
A;Stitle: Genomic cloning and complete sequence analysis of a highly divergent African hu A;Accession: A53034
A;Accession: A53034
A;Status: preliminary
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T14946
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A53034
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A;Tatle: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A;Reference number: Z18268; MUID:99043898; PMID:9826348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T14
R;Lindler, L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y1030 - Yersinia pestis plasmid pMT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 22-Oct-1999
C;Accession: T14946
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A;Molecule type: DNA
A;Residues: 1-402 <HUP>
A;Cross-references: EMBL:AF053947; NID:g2996286; PID:g2996304; PIDN:AAC13184.1
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A; Residues: 1-863 < VAN>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                    Cross-references: GB:L02587
Superfamily: type E retrovirus
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Best Local
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Best Local S
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                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:AF074611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: Y1030
                                                                         672 WLDITKWLWY 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 KORVWYVAPTY 64
                                                                                                          1 WIDIKOFVWY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KQFVWYTPPTF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KOFVWYTPPTF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KORVWYVAPTY 48
                                                                                                                                              s
                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 25;
1; Mismatches
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Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                      env polyprotein
                                                                                                                                              4
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                                                                                                                                                               Score 43; DB
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: 93883003; PID: 93883031; PIDN: AAC82691.1
                                                                                                                                                Mismatches
                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 418;
                                                                                                                                                                                Length 863;
                                                                                                                                              Indels
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A, Cross references: EMBL:X80020; NID:g510516; PIDN:CAA56323.1; PID:g510517
A, Experimental source: isolate VAU
C; Superimental source: isolate VAU
C; Superimental source: isolate VAU
C; Superimental source: solate vAU
C; Superimental source: solate vAU
C; Superimental source: notatin; coat protein; coat protein
C; Keywords: glycoprotein; capsid protein; coat protein
F; 1-30/Domain: signal sequence #status predicted <CFI>F; 31-535/Product: coat protein gp120 #status predicted <CFI>F; 536-877/Product: coat protein gp120 #status predicted <CFI>F; 598-716/Domain: transmembrane #status predicted <TMN>
F; 598-716/Domain: transmembrane #status predicted <TMN>
F; 598-716/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C;Accession: S49197
R;Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy, C submitted to the EMBL Data Library, July 1994
A;Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defire the content of the
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A; Residues: 1-877 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S49197
                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 5
686 WLDITKWLWY 695
                                                                                                                                                                                                                                                 Local Similarity
les 5; Conserv
                                                                                                                        1 WIDIKOFVWY 10
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              46.2%;
                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                                                                       Score 43; DB
Pred. No. 57;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                              DB 2; Length 877; 57;
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Search completed: March 26, 2003, 16:50:42 Job time : 10.5465 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
                                                                                                         A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human six transmem	AAE02780	22	375	100.0	93
Human protein SEQ	AAM79829	22	374	100.0	93
Human P789P protei	ABB95387	23	339	100.0	93
Prostate cancer-as	ABG61813	23	339	100.0	93
P789P amino acid s	AAM01282	22	339	100.0	93
Human protein SEQ	AAM78845	22	339	100.0	93
Human prostate cDN	AAU69927	22	339	100.0	93
Human STRAP-1 prot	AAY58194	21	339	100.0	93
Extracellular loop	AAE02788	22	15	100.0	93
Human STRAP-1 pept	AAY58200	21	15	100.0	93
Description	IĐ	BB	Query Match Length	Query Match	Score

Result No.

4 57	44	43	4 2	41	40	39	38	37	36	35	3 4	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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45.2	ū	ÿ	ÿ	5	ö	6	46.2	9	46.2	•	٥,	9	9	9	46.2		σ,		46.2	47.3	-		47.3	48.4	•	48.4	48.4	48.4	48.4	48.4	48.4	8	50.5	7.
268	268	268	268	268	877	873	873	873	641	474	290	173	171	163	159	148	147	119	62	568	568	403	100	866	861	846	353	353	269	269	268	268	51	339
23	23	19	19	19	17	21	20	20	22	21	22	21	21	19	22	22	23	23	22	22	22	20	22	ø	19	21	17	15	23	19	23	19	22	20
ABG68343	ABG68301	AAY22830	AAY22875	AAY22872	AAW07205	AAY77376	AAY06985	AAY09501	ABB61933	AAY77371	AAU54642	AAU77259	AAU77261	AAW69321	AAG67507	AAG67508	AAG79366	AAU09876	AAU43980	AAU37036	AAU33996	AAW97719	AA004068	AAP80966	AAW43074	AAB69345	AAW02696	AAR48724	ABG68308	AAY22837	ABG68314	AAY22843	AAU21212	AAW86309
Envelope protein g		ID NO	ID NO. 71	ID NO. 68	-1 group O	-1 group		HIV-1 Group O env	Drosophila melanog	HIV-1 group O env	Propionibacterium	Protein ANT70 rela	VAU rela	V-1	Amino acid sequenc	Amino acid sequenc	Zcys7. Homo sapie	Novel human secret	Propionibacterium	Staphylococcus aur	Staphylococcus aur	Staphylococcus aur	Human polypeptide	HIV protein HT7.	HIV-1 gp120 protei	HIV-1 non-subtype	G-protein coupled	t coupled	Envelope protein g		ő	39	fc	ч,

ALIGNMENTS

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AAY58200
IID AAY5
XX
AC AAY5
XX
AC AAY5
XX
AC AAY5
XX
II 14-M
XX
CAL
DE Huma
XX
KW Serg
KW Coval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein.
                                                                                                                                                                                                       01-JUN-1998;
30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                              01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY58200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58200 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9962941-A2
(UROG-) UROGENESYS INC.
(AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                       98US-0087520.
98US-0091183.
                                                                                                                                                                                                                                                                                                                                              99WO-US12157.
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RESULT 2
AAAC02788
ID AAAC0
XX AAAC0
XX AAAC0
XX AAAC0
XX O6-A
XX Extr
XX Huma
XW Six
KW Chro
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                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                   CC entigen of the prostate, ANYSS194). These peptitine transmemorane commonclonal anti-STRAP-I antibodies. STRAP-1 is the prototype commonclonal anti-STRAP family of proteins (AAY58194-Y58197) which commonclonal anti-STRAP family of proteins (AAY58194-Y58197) which commonclonal anti-STRAP family of proteins (AAY58194-Y58197) which commonced in the prototype commonced in the structural conservation, but which show a significant structural homology to known human proteins. The STRAP-1 come significant structural conservation, but which show a common significant structural conservation is a structurally, STRAP-1 is a 339 amino call structurally, STRAP-1 is a thought to be a common significant structurally, STRAP-1 is a 339 amino call structurally structurally structurally structurally, STRAP-1 is a 339 amino call structurally agents, and because they are easily targetted by contains a step structurally structurally agents, and because they are expressed mainly contained side effects on other tissues.
                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic;
                                                                                                          06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAY58198-Y58200 represent synthetic peptides that correspond to the extracellular regions of STRAP-1 (serpentine transmembrane
                                                                    Extracellular loop
                                                                                                                                             AAE02788;
                                                                                                                                                                              AAE02788 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 22; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEON/)
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                                                                                                                                                                                                                                                                                                                                                           Local
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RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                        (first entry)
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                                                                    #3 of human STEAP-1, suitable for cloning into
                                                                                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                             Score 93;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                          4.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and therapeutic targets,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human six transmembrane epithelial CC antigen of the prostate (STEAP) protein. STEAP is a member of cell CC surface serpentine transmembrane antigens. STEAP gene is used in gene CC therapy. Inhibiting the development or progression of a cancer (eg. CC prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP CC or inhibiting growth or killing cells expressing STEAP in a patient, CC comprises administering a vaccine composition to the patient. Treating CC a patient with a cancer that expresses STEAP, or inhibiting growth or CC killing cells expressing STEAP, comprises administering to the patient a CC vector encoding single chain monoclonal antibody that comprises the CC variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the CC that specifically binds to STEAP, such that the vector delivers the CC the encoded single chain monoclonal antibody coding sequence to the cancer cells and CC the encoded single chain monoclonal antibody is expressed CC intracellularly. The present sequence is extracellular loop of STEAP-1 CC suitable for cloning into pFc, which is used in the invention. STEAP-1 CC gene is located on chromosome 7p22.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                  Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; cenbrane protein; expression; cancer; covarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-1999;
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                                                                                                                                                                                                                                                                                                           Human STRAP-1
                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY58194;
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                                                         targetting;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
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Pred. No. 4.3e-07;
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This sequence represents a novel human protein, STRAP-1 (serpentine transmembrane antigen of the proteins (AAY58194-Y58197) which can member of the STRAP family of proteins (AAY58194-Y58197) which carbibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a CC type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane comming, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and
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Region
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                                                                                                                                                                                                                                                                          Novel proteins useful as diagnostic particularly for prostatic cancer
                                                                                                                                                                                                                                                                                                                 N-PSDB;
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DB; AAZ49395, AAZ49396.
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RAITANO A B.
SAFFRAN D C.
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HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                              UROGENESYS INC.
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98US-0091183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local &
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Li SX, Wang A,
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10-OCT-2000;
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29-AUG-2000;
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DB; AAS64160.
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15; Conserv
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GR, Retter MW,
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2000US-0568100.

2000US-0570737.

2000US-0593793.

2000US-0636215.

2000US-0636215.

2000US-0651236.

2000US-0657279.

2000US-0679426.

2000US-0685166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; cytostatic; immunostimulant; tumour; immunogen
                                                                                                                                                                                                                                                                ; Mitcham JL, Harlocker SL, Jiang
er MW, Stolk JA, Day CH, Vedvick
Skeiky YAW, Hepler WT, Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 8.4e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Jiang
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                                                                                                                                                                                                                                                                                               Kalos MD;
Carter D;
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Claim 2; Page

549; 579pp; English.

The invention relates to isolated prostate-specific

human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer.

for

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RESULT 5
AAM/78845
ID AAM/7
AC AAM/7
AC
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-0496914.

27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0625936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                        Tang
Zhao
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                              WPI; 2001-476283/51.
N-PSDB; AAK51978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                         Claim 20; Page 3800-3801; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US04098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM78845 standard; Protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                       ng YT, Liu C, lao QA, Wang D, e AJ, Yang Y, l
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                                                                                                                                                                                                                                                                                                                         Drmanac RT,
), Wang J, Zh
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                            RT, Asundi V,
, Zhang J, Ren
n T, Goodrich R;
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Pred. No. 8.4
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                                                                                                                                                                                                                                                                                                                                  ່ C,
Wang
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ng ZW;
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RESULT 6
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Matches
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                        The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (II), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu J, Dil
Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating e.tivity, tissue growth factor activity, immunomodulatory activity and activity, inthibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-425873/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200151633-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s MD, Fanger GR,
A, Meagher MJ;
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     510-512; 543pp; English.
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Pred. No. 8.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harlocker SL, Jiang Retter MW, Stolk JA,
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Skeiky
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      The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences to them. The prostate cancer associated polynucleotide sequences care differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                              Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                     Gigh
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08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the
                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                N-PSDB; ABK92128.
                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001WO-US32045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG61813;
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                                                                                                                                                                                                                                                                                                                                                              EOSB-)
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gene therapy, as a vaccine or
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                                                                                                                                                                                                                                                                                                            2002-471335/50.
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                                                                                                                                                                                                                                                                                                                                                                                                    -2001;
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                                                                                                                                                                                                                                                                                                                                    Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA;
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2001US-263957P.
2001US-276791P.
2001US-276888P.
2001US-281922P.
2001US-286214P.
2001US-0847046.
2001US-288589P.
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2000US-0733288.
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Best Local Similarity
Matches 15; Conserv
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14-JAN-2000;
27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
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01-AUG-1997;
09-FEB-1998;
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15-JAN-1999;
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                     (XUJJ/)
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(MIL/)
(MIL/)
(HARL/)
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(KALO/)
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(STOL/)
(STOL/)
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14-JUL-1998;
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                    cancer;
WANG A.
SKEIKY Y
HEPLER V
                                                                                              DILLON I
                                                                                      MITCHAM J L.
HARLOCKER S
                                                                                                             r nx
                              CARTER D.
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98US-0020956

98US-0015453

98US-0115453

98US-0115453

98US-012149

99US-0232149

99US-0232149

99US-023216

99US-0439313

99US-0439313

99US-0439313

2000US-0536857

2000US-0536857

2000US-05368100

2000US-05368100

2000US-0536310

2000US-0536310

2000US-0536310
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2000US-0657279.
2000US-0679426.
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W A W.
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Pred. No.
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ID JAM/7
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Best Local
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27-APR-2000; 2000US-0598075.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-062025.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New prostate-specific polynucleotides for diseases, in particular prostate cancer, a progression of cancer -
                                                                                                                                                  Tang YT,
Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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Panger GR, Retter MW,
Li SX, Wang A, Skeik
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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein SEQ ID NO 3475
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                                                                          WPI; 2001-476283/51.
N-PSDB; AAK52962.
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                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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nes 15; Conserv
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                                                                                                                                           Liu C, Drmanac RT, Asundi V,
Wang D, Wang J, Zhang J, Re
Yang Y, Wejhrman T, Goodrich
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MW, Stolk JA, Day CH, Vedvick TS,
keiky YAW, Hepler WT, Henderson RA;
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100.0%; Pred. No. 8.4
tive 0; Mismatches
                                                                                                                                                  Asundi V, Zhou lang J, Ren F, Goodrich R;
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Carter D;
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ng ZW;
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Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human six transmembrane epithelial antigen of prostate (STEAP)-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Immunogenic_peptide
70..91
                                                                                                                                                                                                                                                                                                                                                                                                                                                     158..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= HLA-A2_binding_peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                      /label= HLA-A2_binding_peptide
                                                                                                         /label=
                                                                                                                                                                                                                 label
                                                                                                                                                                                                                                                            abel= Transmembrane_domain #4
                                                                                                                                                          abel= HLA-A2_binding_peptide #3
                                                                                    310
                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                  = HLA-A2_binding_peptide #1
     "Encoded
                                                                                                       Transmembrane_domain #6
                                                                                                                                                                                                           Transmembrane_domain #5
                                                                                                                                                                                                                                                                                                                                                                   Transmembrane_domain #3
                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-A2_binding_peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane_domain #1
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Pred. No. 9.2e-06;
; Mismatches 0;
     by TTGTAGAAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 11
AAW86309
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-1 gene is located on chromosome 7p22.3 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing to the patient. Treating a patient with a cancer that composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody is expressed intracellularly. Note: The present sequence is also shown in sequence listing of the specification, but it lacks amino acid residues at its N-terminal e
                                                                                                                  Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                             01-MAR-1999
                                                                                                                                                                                                                                                                     AAW86309 standard; Protein; 339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 1A-1B; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New STEAP (six transmembrane epithelial antigen of the prostate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD07067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2001.
                                                           WO9853071-A1
                                                                                                                                                                             Kidney injury
                                                                                                                                                                                                                                         AAW86309
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22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                                                                                                                                           1 WIDIKOFVWYTPPTF 15
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                                                                                                                                                                                                                                                                                                                                                WIDIKOFVWYTPPTF 291
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                               associated molecule HW018 protein.
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98WO-US10547.
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 93;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                      9.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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X##X#X#X#######X#X95050505050505050505050505050505
                                                           by expressing KIM encoding polynucleotides, to promote growth and/or CC survival of damaged tissue (e.g. renal tissue), since the KIM proteins CC are upregulated in injured or regenerating (especially renal) tissues. CC KIM fusion proteins, conjugates, antibodies and vectors can also be used CC therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/ CC prophylaxis of conditions associated with disfunction/disregulation of CKIM genes or proteins, especially renal failure, acute nephritis). The CC function in humans (e.g. acute renal failure, acute nephritis). The CC polynucleotides can be used to produce antisense sequences which, when iternalised into cells, can disrupt expression of a cellular KIM gene, CC also useful in therapy (e.g. to block the growth of tumours dependent on CC KIM for growth) or compositions. The proteins and polynucleotides are CC (indicative of increased risk, or presence of, renal injury or impaired CC (useful diagnostically e.g. to detect and quantify renal injury or impaired CC (increased risk, or presence of, an autoimmune response or abnormal CC tissue growth arising from/affecting renal tissue). The proteins can calso be used to locate KIM-producing cells (especially specific loci, ce.g. tissue masses abnormally producing/expressing KIM such as tumours arising from/affecting renal tissue), by contacting cells with an consisting from/affecting renal tissue), by contacting cells with an consisting from/affecting renal tissue).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 57-58; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cate
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23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOJ ) BIOGEN INC.
                                                ımageable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a kidney injury associated molecule M) protein KIM proteins can be administered therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-045312/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hession CA,
                                                KIM-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0047491.
97US-0047490.
                                                reagent and imaging reagent accumulation
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Sequence 339 Ā

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á
                     Query Match
Best Local S
Matches 12
1 WIDIKQFVWYTPPTF 15
                      12;
                              Similarity
                      Conservative
                              87.1%;
80.0%;
                    Score 81; DB Pred. No. 0.000
                     <u>ب</u>
                    DB 20; Length 339;
0.00047;
nes 2; Indels
                      ..
                      Gaps
                      0
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밁
AAU21212;
                AAU21212 standard; Protein;
                                                        277
                                                        WVDISQFVWYMPPTF
                                                        291
                51
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Human novel foetal antigen, SEQ ID NO 1456.

17-DEC-2001

(first entry)

RESULT 12
AAU21212
ID AAU21
XX AU21
XX AU21
XX AU21
XX IT-DE
XX Human
XX Hu immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast nepplasm; cancer; hyperprolative disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischemia; angiogenesis; nervous system disorder; cerebral ischemia; informatical informatica Alzheimer's Human; foetal tissue antigen; antiinflammatory; neuroprotective; disease; infection; ocular disorder; corneal infection

25-SEP-2000; 2000US-0234998. 26-SEP-2000; 2000US-0235464. 27-SEP-2000; 2000US-0235834.	1-SEP-2000; 2000US- 5-SEP-2000; 2000US-	4-SEP-2000; 2000US-	4-SEP-2000; 2000US-	4-SEP-2000; 2000US-	4-SEP-2000; 2000US-	4-SEP-2000; 2000US-	2-SEP-2000; 2000US-	8-SEP-2000; 2000US-	8-SEP-2000; 2000US-	8-SEP-2000; 2000US-	8-SEP-2000; 2000US-	8-SEP-2000; 2000US-	6-SEP-2000; 2000US-	5-SEP-2000; 2000US-	1-SEP-2000; 2000US-	1-SEP-2000; 2000US-	1-SEP-2000; 2000US-	0-AUG-2000; 2000US-	3-AUG-2000; 2000US-	2-AUG-2000; 2000US-	2-AUG-2000; 2000US-	8-AUG-2000; 2000US-	4-AUG-2000; 2000US- 4-AUG-2000; 2000US-	4-AUG-2000; 2000US-	4-AUG-2000; 2000US-	4-AUG-2000; 2000US-	4-AUG-2000; 2000US-	000; 200008-	2000US-	4-AUG-2000; 2000US-	6-JUL-2000; 2000US-	000; 2000US-	1-JUL-2000; 2000US-	7-JUL-2000; 2000US-	7-JUL-2000; 2000US-	0-JUN-2000; 2000US-0	7-JUN-2000; 2000US-	9-MAY-2000; 2000US-	000; 2000US-	000, 2000US-	000; 2000US-	000; 2000US-	000; 2000US-	17-JAN-2001; 2001WO-US01321.	02-AUG-2001.	2	WO200155312-A2.	
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(нима-) нима	PR 11-DEC-2000; 2000US-0254097. PR 05-JAN-2001; 2001US-0259678.	08-DEC-2000; 2000US-02	08-DEC-2000; 2000US-02	08-DEC-2000; 2000US-02	05-DEC-2000; 2000US-02	05-DEC-2000; 2000US-02	01-DEC-2000; 2000US-0250391	01-DEC-2000; 2000US-0250160	17-NOV-2000; 2000US-02	17-NOV-2000; 2000US-0249297	17-NOV-2000; 2000US-0249264	17-NOV-2000; 2000US-0249245	17-NOV-2000; 2000US-0249218	17-NOV-2000; 2000US-0249217	17-NOV-2000; 2000US-0249215	17-NOV-2000; 2000US-0249214	17-NOV-2000; 2000US-0249213	17-NOV-2000: 2000US-0249211	17-NOV-2000; 2000US-0249210	17-NOV-2000; 2000US-0249209	17-NOV-2000; 2000US-0249208	08-NOV-2000; 2000US-0246613	08-NOV-2000; 2000US-0246611	08-NOV-2000; 2000US-0246609	08-NOV-2000; 2000US-0246532	08-NOV-2000; 2000US-0246528	08-NOV-2000; 2000US-0246526	08-NOV-2000; 2000US-0246525	08-NOV-2000; 2000US-0246523	08-NOV-2000; 2000US-0246478	08-NOV-2000; 2000US-0246476	08-NOV-2000; 2000US-0246474 08-NOV-2000; 2000US-0246475	01-NOV-2000; 2000US-0244617	20-OCT-2000; 2000US-0241809	20-OCT-2000; 2000US-0241808	20-00T-2000; 2000US-0241787 20-00T-2000; 2000US-0241787	20-OCT-2000; 2000US-0241785	20-OCT-2000; 2000US-02	13-00T-2000; 2000US-0239937	R 13-OCT-2000: 2000US-0239935	R 02-0CT-2000; 2000US-0237040	R 02-OCT-2000; 2000US-0237038	R 02-OCT-2000; 2000US-02	29-SEP-2000; 2000US-02:	R 29-SEP-2000; 2000US-02:	R 29-SEP-2000; 2000US-02:	29-SEP-2000; 2000US-02:	

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RESULT 13
AAY22843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel nucleic acids encoding novel human foetal CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g. CC by gene therapy) or amellorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated cinclude autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC be used to aid wound healing and epithelial cell proliferation, to CC resemblation, for supporting cell culture of primary tissues, to CC resemblation, for supporting cell culture of primary tissues, to crass food additive or preservative to increase or decrease storage considerals, cofactors and other nutritional components. Numerous and disorders referred by the nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                        HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine; antibody; viral membrane fusion; viral infectivity; ligand affinity purification; protein A replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
                                    16-JUN-1997;
06-NOV-1996;
                                                                                                05-NOV-1997;
                                                                                                                                                                                                              Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY22843 standard; Protein; 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID No 1456; 642pp; English
                                                                                                                                                                           WO9820036-A1
                                                                                                                                                                                                                                                     immunoglobulin purification; epitope mimic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory systems
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 WFDLQQFSFYCPLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WIDIKQFVWYTPPTF 15
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of diseases and disorders treated by the nucleic acids and are given in the specification. The present sequence
                                                                                                                                                                                                                                                                                                                                                         39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                       from WO9820036.
                                    97US-0876698.
96US-0743698.
                                                                                              97WO-US20069
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46.7%;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                16-JUN-1997;
06-NOV-1996;
16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of constrained helical peptide(s) by linking side chains on termini of octa:peptide - derived from human immunodeficiency
                                                                                                                                        07-AUG-2001.
                                                                                                                                                                           US6271198-B1
                                                                                                                                                                                                         Human immunodeficiency virus type 1 clade
                                                                                                                                                                                                                                                            HIV; glycoprotein; gp41; antigen; helical conformation;
virus-induced membrane fusion; acquired immunodeficiency
                                                                                                                                                                                                                                                                                                              Envelope protein gp41 from HIV clade B strain #33.
                                                                                                                                                                                                                                                                                                                                                  07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                    ABG68314;
                                                                                                                                                                                                                                                                                                                                                                                                                      ABG68314 standard; Protein; 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus (HIV). Specifically, AAY22810-Y22910 are Antima from ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 180-181; 279pp; English
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Wells JA;
                                                                                                      05-NOV-1997;
 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                           envelope protein; vaccine;
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nilarity 60.0%;
Conservative
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                                97US-049787P.
96US-0743698.
97US-0876698.
                                                                                                        97US-0965056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptides or proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 45; DB; Pred. No. 69; 2; Mismatches
                                                                                                                                                                                                                                             virucide; anti-HIV
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                                                                                                                                                                                                                                                               syndrome;
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WPI; 1998-286866/25

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ID AAY22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine; antibody; viral membrane fusion; viral infectivity; ligand affinity purification; protein A replacement;
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                                             Braisted A,
Wells JA;
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06-NOV-1996;
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                                                                                                                                                             (GETH ) GENENTECH INC.
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96US-0743698.
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69; 19; ν ••

Length 269; Indels

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Gaps

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Sequence

269 AA;

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CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and CC AAY22903 represent consensus sequences of various sections of the gp41 CC protein). Sequences derived from the peptides are used to produce CC constrained helical peptides of the invention. The constrained helical peptides of the invention. The constrained helical cc amino acids have a side-chain that includes a group able to form an amide cc bond, and cyclising the octapeptide by reacting the specified side-chain cc residues with a diffunctional linker to produce two amide bonds. CC infection, especially as vaccines that generate antibodies that CC constrained helical peptides are used to treat or prevent HIV cc infection, especially as vaccines that generate antibodies that CC constrained helical peptides derived from several different strains of CC constrained helical peptides derived from several different strains of CC uses for the constrained helical peptides are in affinity purification of ligands (particularly where complete binding protein is not readily cc available, e.g. replacements for protein A in immunoglobulin cc forms of "floppy" peptides or protein A in immunoglobulin cc of synthetic antibody clones from phage display libraries, or as stable cc forms of "floppy" peptides or proteins.
Production of constrained helical peptide(s) by linking side chains on termini of octa:peptide - derived from human immunodeficiency virus gp41 protein, useful in vaccines for treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins
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Search completed: March 26, 2003, 16:48:16 Job time: 30.1279 secs 밁 203 WEDITOWLWY 212

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Result
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142.679 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
   GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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Q9uhe8 homo sapien Q92375 rhizobium m p04579 human immun Q01371 neurospora Q42266 ictalurus p p46992 saccharomyc Q9epq1 mus musculu p19550 human immun p53721 saccharomyc p7128 escherichia O32140 bacillus su p14297 manduca sex p35961 human immun p17281 chimpanzee p05881 human immun p17281 clostridium p20755 oryctolagus p05880 human immun p14487 human immun p14946 lolium pere p43213 phleum prat p3196 homo sapien Q3119 homo sapien Q3125 haemophilus Q58015 methanococc Q51861 methanococc
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SOT FIT KWR

Transmembrane;

EMBL; AF186249; AAF17479.1; EMBL; AC005053; AAC79150.1; EMBL; AC004969; AAD15620.1; EMBL; BC011802; AAH11802.1;

ALT_INIT.

Genew; HGNC:11378; STEAP MIM; 604415; -

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361 1 SERC BACHD 459 1 NUJ4M_MACRO 847 1 MDOH_ECOLI 868 1 ENV_HVIEL 868 1 ENV_HVIEL 868 1 ENV_HVIEL 868 1 ENV_HVIEL 1000		email	d this	m-prof	e Swis	PROT e		SPECTS	10L-20	7.	15	OM N.A		JUN-19	OM N.A	:	Acad.	rostat	A., Sa	C., Mai	, Viva	56277;	Ž Z	9606;	utheri	Meta70	EAP1	mbrane	(Rel .	(Rel.	034;	ST				4 C.	40.9	40.9	40.9	40.9	41.9	41.9			
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Capela D., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

Godfie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

--- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

FOR ALPHA-GLUCOSIDES SUCH AS SUCROSE, MALTOSE AND TREHALOSE.

--- SUBCELLULAR LOCATION: Periplasmic (Probable).

--- SUBCELLULAR EDENORS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGLE_RHIME
Q9Z3R5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as long as its content use for profit institutions as lo
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MEDLINE=9938961; PubMed=10400573;

Willis L.B., Walker G.C.;
"A novel Sinorhizobium meliloti operon encodes an alpha-gluco and a periplasmic-binding-protein-dependent transport system alpha-glucosides";
J. Bacteriol. 181:4176-4184(1999).
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15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-glucosides-binding periplasmic protein
AGLE OR R00695 OR SMC03061.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
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Pred. No.
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13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprocein GP160 precursor (Contains: E
glycoprotein (GP120); Transmembrane glycoprotein
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Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., We
"Identification and characterization of conserved a
regions in the envelope gene of HTLV-III/LAV, the I
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HIV; M17451; ENV$RF.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

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                                                                                                                                                                   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR INVOLVED IN LIGHT REGULATION OF THE AL-3
GENE. WC1 AND WC2 PROTEINS INTERACT VIA HOMOLOGOUS PAS DOMAINS,
BIND TO PROMOTERS OF LIGHT REGULATED GENES SUCH AS FRQ, AND
                             use
                                                                                                                                                                                                                                                                                        STRAIN=74-OR23-1A;
MEDLINE=96203083; PubMed=8612589;
Ballario P., Vittorioso P., Magre
         modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                     Ballario
                                                                                                                                                                                                                                                   ЕМВО J.
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                             White collar
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16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                           "White collar-1, a central regulator of blue light responses Neurospora, is a zinc finger protein.";
                                                                                                                                                                                                                                                                                  Macino G.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                           ACTIVATE TRANSCRIPTION.
SUBUNIT: HETERODINER OF WC1 AND WC2 (POTENTIAL).
SUBCELLULAR LOCATION: Nuclear.
INDUCTION: BY BLUE LIGHT.
INDUCTION: BY BLUE LIGHT.
DOMAIN: THE GLUTAMINE-RICH DOMAIN MIGHT FUNCTION IN ACTIVATING GENE EXPRESSION.
SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 3 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 2 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAINS.
                                    ween the Swiss Institute of Bioinf.
European Bioinformatics Institute.
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15:1650-1657(1996).
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ZN FING
                                                                                                                  Blackshaw S., Snyder S.H.;

"Parapinopsin, a novel catfish opsin localized to the parapineal organ, defines a new gene family.";

J. Neurosci. 17:8083-8092(1997).

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: PARAPINEAL ORGAN.
                                                                                                                                                                                                                     Ictalurus punctatus (Channel catfish).
Eukaryota, Metazoa; Chordata; Craniata;
Actinopterygii, Neopterygii; Teleostei;
Ictaluridae; Ictalurus.
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SMART; SM00091; PAS; 3.
SMART; SM000401; ZnF_GATA; 1.
TIGREAMS; TIGR00229; sensory
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15-JUL-1998 (Rel. 36,
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PROSITE; PS50114; GATA ZN FINGER 2; 1.
PROSITE; PS50112; PAS; 3.
Transcription regulation; Activator; Di
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Pfam; PF00785; PAC; 2.
Pfam; PF00989; PAS; 3.
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                                                                                                                                                                              MEDLINE=97477428; PubMed=9334384;
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                           s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL Buropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                            SIMILARITY: BELONGS OPSIN SUBFAMILY.
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P17679; IGNF.
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Pred. No. 27;
2; Mismatches
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PAS 1.
PAC 1.
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Ostariophysi; Siluriformes;
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P46992;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 43.0 kDa protein in CPS1-FPP1 intergenic region.
YJU171C OR JOS12.
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PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1 1;

PROSITE; PS00238; GPROTEIN_RECEP_F1_2;

PROSITE; PS00238; OFSIN; 1.
                     EMBL;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Obermaier B., Piravandi E., Rinke M., Domdey H
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ
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                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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S0003707; YJL171C.
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l; Mismatches
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Pred. No.
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4 (POTENTIAL).
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  Palmitate; G-protein coupled r
  EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL)
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3 (POTENTIAL).
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(GLCNAC. . .) (P
E (BY SIMILARITY)
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CCPRARA A REPRESENTANT OF THE SECOND 
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 09, Created)
15-JUL-1998 (Rel. 09, Last sequence update)
15-JUL-1998 (Rel. 09, Created)
15-JUL-199
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SEQUENCE FROM N.A.
MEDLINE=87219095; PubMed=3556215;
Ter-Avanesyan M.F.
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SEQUENCE FROM N.A.
MEDLINE=88296422; PubMed=2841115;
MEDLINE=88296422; PubMed=2841115;
MEDLINE=88296422; PubMed=2841115;
translation termination in Saccharomyces cerevisiae EMBO J. 14:4365-4373(1995).
-i- FUNCTION: INVOLVED IN TRANSLATION TERMINATION.
ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
                                                                                                                     MEDLINE=96016209; PubMed=7556078; Stansfield I., Jones K.M., Kushnirov V.V., Poznyakovski A.I., Paushkin S.V., Nierras C Ter-Avanesyan M.D., Tuite M.F.; "The products of the SUP45 (eRF1) and SUP3:
                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / AB972;
Murphy L., Harris D.E.,
Submitted (NOV-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A yeast gene required for the Gi-to-S containing an A-kinase target site and EMBO J. 7:1175-1182(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson P.G., Culbertson M.R.;
"SUFILS suppressor protein of yeast...
EF-1 family of elongation factors.";
J. Mol. Biol. 199:559-573(1988).
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MEDLINE=88329727; PubMed=3047009;

Kushnirov V.V., Ter-Avanesyan M.D., Telckov M.V.,

Smirnov V.N., Inge-Vechtomov S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=88172503; PubMed=3280807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Localization of possible functional domains the yeast Saccharomyces cerevisiae."; FEBS Lett. 215:257-260(1987).
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                                                                                                                                                                                                                                                                                              FUNCTION
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InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTbbind.
Pfam; PR00009; GTP_EFTU_D3; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                        TIRI MOUSE STANDAND,

TIRI MOUSE STANDAND,

QSEPQI; QSEPWS;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)
receptors.";
Proc. Natl. 1
[2]
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                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUB=Macrophage;
MEDLINE=20558581; PubMed=11095740;
Ozinsky A., Underhill D.M., Fontenot J.D.,
Wilson C.B., Schroeder L., Aderem A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M21129; AAA35133.1; -. EMBL; X07163; CAA30155.1; -. EMBL; Y00829; CAA68760.1; -. EMBL; Z46727; CAA86677.1; -.
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                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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SGD; S0002579; SUP35.
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SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDPKECPWYTGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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Rodentia;
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TO ELONGATION FACTORS EF-1.

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

INTERACT WITH GTP/GDP (BY SIMILARITY).

INTERACT WITH GTP/GDP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).
                                                           recognition cooperation
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Pred. No.
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                                                                                                                                                                                                                                               Craniata; Veri
Sciurognathi;
                       97:13766-13771 (2000)
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                                                           of patho
                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                           pathogens by t
tween Toll-like
                                                                                                                       Hajjar A.M.,
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Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;
Thomson D.P., Campbell Toll-like receptor 1.";
"Cloning of Mus musculus Toll-like receptor 1.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00370; LRR; 3.
SMART; SM00382; LRRCT; 1.
SMART; SM00369; LRR TYP; 6.
SMART; SM00255; TIR; 1.
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MEDLINE=20571875; PubMed=11123271;
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Pfam; PF01582; TIR; 1
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InterPro; IPR000483; LRR Cterm.
InterPro; IPR003592; LRR_typ.
InterPro; IPR003591; LRR_typ.
InterPro; IPR000157; TIR_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00560; LRR;
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SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 TIR DOMAIN.
SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Participates in the innate immune response to microbi agents. Cooperates with TLR2 and modulates the response to microbial constituents. Acts via MyD88 and TRAF6, leading to NF kappa-B activation, cytokine secretion and the inflammatory response (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane because in the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY009154; AAG37302.1;
AF316985; AAG35062.1;
O60603; IFYW.
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TOLL-LIKE RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
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Best Local &
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Signal.
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p19550;
01-FEB-1991 (Rel. 17, Create
01-FEB-1991 (Rel. 17, Last s
15-JUL-1999 (Rel. 38, Last s
Envelope polyprotein GP160 p
glycoprotein (GP120); Transm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid
NCBI_TaxID=11691;
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GP160 precursor [Contains: Exterior membrane
Transmembrane glycoprotein (GP41)].
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Pred. No. 33;
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Pohl T.M.;
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                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCAD_ECOLI STANDARD; PRT; 405 AA. P71238; P76385; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative colanic acid polymerase.
                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-i- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                             Lipopolysaccharide biosynthesis; Complete proteome.
CONFLICT 108 108 P -> A (IN REF. 2).
SEQUENCE 405 AA; 45409 MW; A3D9D91255686043 CRC64;
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between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12;
Reeves P.R.
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RA Kunst F. Ogsawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursher L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Abaret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Lazer R., Galigron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Aloris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oodega B., Park S. H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Rocha E., Rocha B., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Visati A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Ray Vishia K., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Ray Vishia K., Wambutt K., Wedler E., Wedler H., Weitzeneger T.,
Ray Vishia K., Wambu
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Schultz A.C., Nygaard P., Saxild H.H.;
Schultz A.C., Nygaard P., Saxild H.H.;
"Functional analysis of 14 genes that constitute the public pathway in Bacillus subtilis and evidence for a novel controlled by the Puck transcription activator.";
J. Bacteriol. 183:3293-3302(2001).
J. FUNCTION: Uptake of uric acid.
1- FUNCTION: Uptake of uric acid.
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SubtiList; BG13985; puck.
TherPro; IPR000444; Xan ur permease; 1.
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Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Pfam; PF00372; hemocyanin_C; 1.
Pfam; PF003723; hemocyanin_C; 1.
PFAM; PF003723; hemocyanin_C; 1.
PRINTS; PR00187; HAEMOCYANIN.
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TISSUE-Larval fat body;
MEDLINE-90037032; PubMed=2808410;
Willott E., Wang X.-Y., Wells M.A.;
"CDNA and gene sequence of Manduca sexta arylphorin,
"CDNA and gene sequence of Manduca sexta arylphorin,
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PROSITE; PS00210; HEMOCYANIN_2; 1.
Signal; Storage protein; Glycoprotein; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Arylphorin beta subunit precursor.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda
Insecta; Peerygota; Neptrera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI TaxID=7130;
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P14297;
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EMBL; M28397; AAA29305.1; -.
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Matches
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PIR, H44001; H44001.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glyc Signal.
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15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: E
glycoprotein (GP120); Transmembrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence, genome organization, properties of human immunodeficiency virus type 1 if for limited defectiveness and complementation."; J. Virol. 66:6587-6600(1992).
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MEDLINE=9301387; PubMed=1404605;
Li Y., Hui H., Burgess C.J., Price R.W.,
Shaw G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement or send an email to license@isb-sib.ch
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No.
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ENV_SIVCZ
ENV_SIVCZ
P17281;

01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane Envelope polyprotein (GP160); Transmembrane glycoprotein (GP41)].
Pfam; PF00516; C
Pfam; PF00517; C
AIDS; Coat Prote
Signal. 1
SIGNAL 1
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PIR; 9
HIV; 3
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G.,
"Genetic organization of a chimpanzee lentivirus
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                 Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11723;
                                                                                        InterPro;
InterPro;
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                                                                                                                                                    X52154; CAA36407.1; -.
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Pred. No.
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Q9upn3 homo sapien
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p31627 caprine art
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RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Honfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Caratton M., Dear S., Du Zi, Durbin R., Favello A., Fraser A.,

RA Chiton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,

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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE00409.
                                                                                                                                                                                                                                                                                                                                                                      30.5%;
43.5%;
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159237 MW; 4FC83B9E7ADF7788 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      Score 58.5;
Pred. No. 5.
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                                                                                                                                                                                                     EMBL; U13979; AAA73513.1; -.
EMBL; Z99122; CAB15585.1; -.
Subtilist; BG11192; ggaB.
InterPro; IPR001173; Glycos transf_2.
Pfam; PF00535; Glycos transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 900 AA; 107154 MW; FA66495488C2C62F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       we by non-profit institutions as long as its content is in entitles requires a license agreement.
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borche
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted by the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
-I- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING MINOR TEICHOIC ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                      Similarity
                                                                      Conservative
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                                                                                                  30.2%;
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                                                                                                      Score
Pred.
                                                                      Mismatches
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                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
   34
                                                                                                                                      DB 1;
                                                                                                                                      Length 900;
                                                                                                                                                                                                                CRC64;
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Borchert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by and for commercial
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOKC_BAC
P54566;
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SEQUENCE
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P55377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Hypothetical protein; Plasmid; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
sporulation genes.";
Microbiology 142:3103-3111(1996)
[2]
                                                                                                                                                          STRAIN=168 / JH642;
MEDLINE=97124195; Po
                                                                                                                                                                                                                                                                                                                                  Hypothetical YQKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97305956; PubMed=9 Freiberg C.A., Fellay R.,
                                                                    "Systematic sequencing of the 283 kb the Bacillus subtilis genome containi
                                                                                                                   Mizuno M., Ma
Kobayashi Y.;
                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                         Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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                                                                                                                                                                                                                                                          NCBI_TaxID=1423;
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630 AA;
                                                                                                                                         Masuda S.,
                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
(Rel. 34, Last sequence update)
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1 protein yqkC.
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llay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                       PubMed=8969508;
S., Takemaru K.-I.,
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; 67854 MW;
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                                                                    genome containing the
                                                                                                                                                                                                                                                                                     Bacillales;
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Pred. No. 8.5;
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                                                                                                                                         Hosono S.,
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                                                                                                                                         Takeuchi M.,
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OS Caenor
OC Eukary
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RP SEQUEN
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ginesphi G., Guy B.J., Haga K., Halsch J., Harwood C.R., Henaut A.,
RA Glisephi G., Guy B.J., Haga K., Halsch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Miners D., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
"The complete genome sequence of the Gram-positive bacterium Bacillus
RT subrilis ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches
                                                                                                                                          UNI3 CAEEL STANDARD; PRT; 1813 AA P27715; 017665; Q23512; 01-AUG-1992 (Rel. 23, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phorbol ester/diacylglycerol-binding protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D84432; BAA12635.1; -.
EMBL; Z99116; CAB14297.1; -.
SubtiList; BG11758; yqkC.
Hypothetical protein; Complet
SEQUENCE 79 AA; 9287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=168;
    SEQUENCE FROM N.A.
                                                                                                      UNC-13 OR ZK524.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
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                                                                   Rhabditidae;
                                                                                       Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                              2 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRME
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                                                                   Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in; Complete proteome 9287 MW; 34852BDAEA
    (ISOFORM
                                                                                     Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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28.1%;
                                                                   Caenorhabditis
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B; Mismatches
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STRAIN-Bristol

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EMBL; 292779; CAB07173.1; J. EMBL; 279694; CAB07173.1; J. GEMBL; 273912; CAB07173.1; J. GEMBL; 273912; CAB98146.1; EMBL; 273912; CAB98147.1; J. GEMBL; 279694; CAB98147.1; J. GEMBL; 279694; CAB98147.1; J. GEMBL; 27979; CAB01966.1; EMBL; 27979; CAB01966.1; GEMBL; 273912; CAB01966.1; J. GEMBL; 273912; J. GEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system.
Mol. Biol. Cell
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                        WormPep; ZK524.2a; CE15371.
WormPep; ZK524.2b; CE15287.
InterPer; IPR000008; CZ PE-bind.
InterPro; IPR002219; DAG PE-bind.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00168; C2; 3.
                                                                                                                                                                                                                                                 PIR;
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Gardner A.E., Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20483775; PubMed=11029047;
Kohn R.E., Duerr J.S., McManus J.R., Duke
Moulder G., Maruyama I.N., Barstead R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maruyama I.N., Brenner S.;
"A phorbol ester/diacylglycerol-binding protein encoded by
                           PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M62830; AAA93094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene of Caenorhabditis elegans.";
Proc. Natl. Acad. Sci. U.S.A. 88:5729-5733(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93075060; PubMed=1445255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of multiple UNC-13 proteins nervous system.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROTRANSMITTER FROM NEURONS:
ALTERNATIVE PRODUCTS: 4 isoforms; 1/ZK524.2a (8 and 4/ZK524.2b; may be produced by alternative DOMAIN: THE PHORBOL ESTER BINDING ACTIVITY IS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed S., Maruyama I.N., Kozma R., Lee J., Brenner S., Lim L.
e Caenorhabditis elegans unc-13 gene product is a phosphol
endent high-affinity phorbol ester receptor.";
chem. J. 287:995-999(1992).
FUNCTION: MAY FORM PART OF A SIGNAL TRANSDUCTION PATHWAY,
TRANSDUCING THE SIGNAL FROM DIACYLGLYCEROL TO EFFECTOR
FUNCTIONS. ONE SUCH FUNCTION COULD BE THE RELEASE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 3 C2 DOMAINS.
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SIMILARITY: CONTAINS 1
BINDING DOMAIN.
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MISCELLANEOUS: MUTATIONS IN UNC-13 CAUSE DIVERSE NERVOUS SYSTEM
                                                                                                                                                                                                                                              A41101; A41101.
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                                                                                                                                                                                                                     P28867; 1PTQ.
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R.J., Rand
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product is a phospholipid-
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Rand J.B.;
the Caenorhabditis elegans
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RESULT 7
GLPK_SYNY3
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Phorbol-ester bindi
DOMAIN 21
DOMAIN 693
DOMAIN 802
DOMAIN 1633
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CONFLICT
SEQUENCE
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VARSPLIC
                                                                                                                                                                                                                                                                                                                      MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Agamizu E., Nakamura Kaneko T., Sato S., Kotani H., Tanaka A., Sasamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3
(Glycerokinase) (GK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strai)
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00239; C2; 3.
PROSITE; PS00499; C2_D
PROSITE; PS50004; C2_D
PROSITE; PS00479; DAG_
PROSITE; PS00479; DAG_
                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLPK OR SLR1672
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                                                                                                      CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate PATHMAY: Glycerol utilization; rate-limiting step. SIMILARITY: BELONGS TO THE FUCCKINASE / GLUCONOKINASE / GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                 FUNCTION:
                                                                                                                                                                                             METABOLISM.
               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNY3
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## C2 DOMAIN 2; 2.

## DAG PE BIND DOM 1; 1.

## P850081; DAG PE BIND DOM 2; 1.

## P850081; DAG PE B
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C2 DOMAIN 2.
C2 DOMAIN 3.
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Pred. No.
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MISSING (IN ISOFORM 4).

DNEKDIWKOHVEGYEEGOEEKOKDNOKPNDHSAASPODHYH

RSDSTAOODFGNNIVROTIOEEEEKRNYOELMHNAYKRVCA

DLGI -> MPRRRKRKRVKIKKSRSCPILMKTEKTPHPMKS
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5; Mismatches
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SYVTVKLQTVKSTTVAVRGNLPCWEQEFIFETNRPDDG
MVLELWAKG -> MGQR (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Alternative splicing C2 DOMAIN 1.
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52;
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                                                                                                                                                                                                                      GLYCEROL UPTAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amportation update)
Potential calcium-transporting ATPase 13, plasma membrane-type
(EC 3.6.3.8) (Ca2+-ATPase, isoform 13).
ACA13 OR AT3G22910 OR FSN5.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY C; 1.
TIGRFAMS; TIGR01311; glyc
                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
EMBL; AP001300;
HSSP; P04191; 11
                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LIK7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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                                                                                                                                                                                                                                                                                           Res. 7:217-221(2000).

FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE TRANSLOCATION OF CALCIUM FROM THE CYTOSOL OUT OF THE CELL OR INTO ORGANELLES (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+)(In) = ADP + phosphate +
                                                                                                                                                                               BINDING DOMAIN, WHICH BINDS CALMODULIN IN A CALCIUM-FASHION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES
                                                                                                                                                                                                               ENZYME REGULATION: ACTIVATED BY CALMODULIN (BY SIMILARITY). SUBCELLULAR LOCATION: Integral membrane procesin. DOMAIN: THE N-TERMINUS CONTAINS AN AUTOINHIBITORY CALMODULIN-BINDING DOMAIN, WHICH BINDS CALMODULIN IN A CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                        BAC clones."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TIGR01311; glycerol kin; 1
PS00933; FGGY_KINASES_1; FAI
PS00445; FGGY_KINASES_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and this statement is not removed requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolism; Transferase;
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                                                                                                                                                                  ATPASES). SUBFAMILY IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columbia;
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 IEUL.
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                BAB03036.1;
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                                                                                     as
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Best Local S
Matches
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InterPro; IPR004014; Cation_ATPase.
InterPro; IPR001454; Hlgnase/hydrlase.
Pfam; PP00122; E1-E2 ATPase; 1.
Pfam; PP00689; Cation_ATPase_C; 1.
Pfam; PP00690; Cation_ATPase_N; 1.
Pfam; PP00702; Hydrolase; 1.
                                                                                                                                                                                         Q9Y705;
16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat spindle pole body component alp4.
ALP4 OR SPBC365.15.
                                                                                                                                                                                                                                                                                                                                                                                       METAL
SEQUENCE
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MOD_RES
METAL
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TRANSMEM
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DOMAIN
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PROSITE; PS00154; ATPASE_E1_E2; 1.

Hydrolase; Calcium transport; Transmembrane; Phosphorylation; ATP-binding; Metal-binding; Magnesium; Calmodulin-binding; Multigene family; Hypothetical protein.

1 147 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                        ALP4
                    "The fission yeast gamma-tubulin complex is required is a component of the spindle assembly checkpoint."; EMBO J. 19:6098-6111(2000).
                                                      MEDLINE=20532503; PubMed=11080156;
Vardy L., Toda T.;
                                                                                                                       Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
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SEQUENCE FROM N.A.
                                                                                       SEQUENCE FROM N.A.,
                                                                                                           NCBI_TaxID=4896;
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169
187
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                       STANDARD;
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                                                                                       AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                      26.6%;
34.6%;
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Pred. No.
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PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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                                           in G(1) phase
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RESULT 10
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RA Bgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gonlles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Oliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Gorrow R., Langer I., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Garbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Gord R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Gord R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Gord R.R., Cruzado J., Barrell B.G., Nurse P.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Gord R.R., Collet B., Barrell B.G., Nurse P.,
RA Gord R.R., Collet B., Barrell B.G., Nurse P.,
RA Gord R.R., Collet B., Barrell B.G., Nurse P.,
RA Gord R.R., Collet B., Barrell B.G., Royala R.R., Collet B.,
RA Gord R.R.
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Best Local Similarity
                                                                                                                                                                                                                                                   Tayll RAT STANDARD; PRT; 1574 AA.

(62910; Q62911; O80992;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Synaptojanin 1 (EC 3.1.3.56) (Synaptic inositol-1,4,5-trisphosphate phosphatase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL078627; CAB44767.1; -. EMBL; AB026664; BAA77269.1; -. Microtubules; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercian
   SEQUENCE
                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
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SIMILARITY: BELONGS TO THE GCP FAMILY.
   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
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   (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90157 MW;
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Pred. No.
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Sciurognathi;
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                                                                                                          Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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MEDIATED ENDOCYTOSIS.

***MEDIATED ENDOCYTOSIS.**

***INCLIDED TO ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + (2)0 = D-myo-inositol 1,4-bisphosphate + phosphate.**

**D-myo-inositol 1,4-bisphosphate + phosphate.**

**SUBCELULLAR LOCATION: LOCALIZED MAINLY IN THE SOLUBLE FRACTION (BY SIMILARITY).**

**PATISON JINOSPHATE SUBJECTION IN POSITION 1309 IS SUPPRESSED IN ISOPORM 3, BY IS ALIOPORMS.**

**PATISON SPECIFICITY: ISOPORM 1 IS POUND IN NEONATAL BRAIN, AND IN A WIDE VARIETY OF ADULT NON-NEURONAL TISSUES. ISOPORM 2 IS EXPRESSED PREDOMINANTLY IN THE NEURONS, BUT IS ALSO FOUND IN ALL OTHER TISSUES AT MUCH LOWER LEVELS. ISOPORMS 1 AND 2 ARE DETECTED IN THE LUNG AND HEART. ISOPORM 1 IS EXPRESSED AT HIGHER LEVELS. THAN ISOPORMS 3 MITH THE 16-AMINO-ACID INSERT IS ONLY FOUND IN THE BRAIN WHILE ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS POUND IN THE LUNG.**

**PEUDOMONANT BY SHORT AND BOTH ISOPORM 3 MITHOUT THE 16-AMINO-ACID INSERT IS
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramjaun A.R., McPherson P.S.; Tissue-specific alternative splicing generates two synaptojanin interferential membrane binding properties."; J. Biol. Chem. 271:24856-24861(1996).
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Grabs D., Sossin W.S., Bauerfeind R., Nemoto
"A presynaptic inositol-5-phosphatase.";
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                                                                                                                                     or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                         DOMAIN: THE C-TERMINAL PROLINE-RICH REGION MEDIATES VARIETY OF SH3 DOMAIN-CONTAINING PROTEINS INCLUDING SH3P4, SH3P8, SH3P13 AND GRB2.

DOMAIN: SPLICING OF THE SAC1 DOMAIN DOES NOT ALTER TACTIVITY OF SYNAPTOJANIN 1.

SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE ITRISPHOSPHATE 5-PHOSPHATASE FAMILY.

SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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                                                                                                                                                                                                                                                                                                                                                                                                     TO THE INOSITOL-1,4,5
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EMBL; U45479; AAB60525.1; -.
EMBL; U45479; AAB60526.1; -.
EMBL; AJ006855; CAA07267.1;
InterPro; IPR005135; Exo_end

.1; ALT_TERM. _endo_phos.

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90UPN3; Q9UKP0; Q9ULPG9; Q9H540; O75053;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Actin cross-linking family protein 7 (Macrophin)

(620 kDa actin-binding protein) (ABP620).

ACET OR ABP620 OR KIAA0465 OR KIAA1251.
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DOMAIN
                                                                                          MEDIINE=20026884; PubMed=10559237; Sun Y., Zhang J., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y., Suntherland R., Saleta R., Griffin J.D., Ferland L.H., Chen L.B.; "Molecular cloning and characterization of human trabeculin-alpha, giant protein defining a new family of actin-binding proteins."; J. Biol. Chem. 274:33522-33530(1999).
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=20001959; PubMed=10529403;

MEDLINE=20001959; PubMed=10529403;

Medida T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,

Takahashi M., Ishigaki T., Hamaguchi M.;

Takahashi M., Ishigaki T., Hamaguchi M.;

"Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin.";

Richard Medida T., Iwahashi N., Ishigotani M., Ishigotani M., Ishigotani M., Ishigotani M., Ishigotani M., Ishigotani M., Ishigotani Y., Iwahashi N.,

"Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin.";

Richard M., Ishigotani Y., Iwahashi N.,

"Mahashi N.,

"Mahashi N.,

"Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin.";

Richard M., Ishigaki T., Hamaguchi M., Ishigatani Y., Iwahashi N.,

"Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin.";

Richard M., Ishigatani M., Ishigatan
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Pfam; PF03372; Exo_endo_phos;
SMART; SM00128; IPPc; 1.
                                     SEQUENCE OF 868-2350 FROM TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Alternative splicing; Repeat; Endocytosis; RNA-binding;
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InterPro;
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                 MEDLINE=20039619; PubMed=10574462;
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IPR002013; Syja_N.
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Ishikawa K.-I., Kikuno R.,
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Pred. No. 83;
8; Mismatches
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3 X 3 AA REPEATS
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(IN REF. 2).
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 Hirosawa M.,
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83;
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N 16AA INSERTLESS ISOFORM).
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REF. 1; AAB60525).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Trabeculin-alpha)
 Nomura
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Pfam; PF002187; GAS2; 1.
ProDom; PD000012; EF-hand; 1.
SMART; SM00033; CH; 2.
SMART; SM00054; EFh; 2.
SMART; SM00054; EFh; 2.
SMART; SM00243; GAS2; 1.
SMART; SM00150; SPEC; 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohara O.; "Prediction of the coding sequences The complete sequences of 100 new CD for large proteins in vitro."; DNA Res. 6:337-345(1999).
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Seki N., Ohira M., Nagase T., Ishikawa
Nakajima D., Nomura N., Ohara O.;
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TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 ACTIN-HOMOLOGY (CH) I
SIMILARITY: CONTAINS 2 EF-HAND CALCUM-BINDING
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 37 SPECTRIN REPEATS.
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PUNCTION: F-ACTIN-BLIDING PROTEIN WILLINKING ACTIN TO OTHER CYTOSKELETAL MICROTUBULES (BY SIMILARITY).
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L; AF141968; AAF06360.1; -.
L; AB033077; BAA86565.1; -.
L; AL137853; CAC15920.1; -.
L; AB007934; BAA32310.1; -.
L; AB007934; BAA32310.1; -.
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o; IPR001715; Calponin-like.
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o; IPR001452; SH3.
o; IPR002017; Spectrin.
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C --- CATALYTIC ACTIVITY: SUCCINY1-COA + 2,3,4,5-tetrahydropyridine-2-C C --- CATALYTIC ACTIVITY: SUCCINY1-L-2-amino-6-oxoheptanedioate.

C --- CATALYTIC ACTIVITY: SUCCINY1-L-2-amino-6-oxoheptanedioate.

C --- PATHWAY: FOUNTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND LYSINE FROM ASPARTATE SEMIALDEHYDE.

C --- SUMCELLULAR LOCATION: CYCOplasmic (By similarity).

C --- SIMILARITY: BELONGS TO THE CYSE/LACA/LEXA/NODL FAMILY OF ACTIVITY: BELONGS TO THE CYSE/LACA/LEXA/NODL FAMILY OF ACTIVITY OF ACTI
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Hypothetical protein; Plasmi
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P57323;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase

(EC 2.3.1.117) (Tetrahydrodipicolinate N-succinyltransferase)

(THP succinyltransferase) (Tetrahydropicolinate succinylase).

DAPD OR BUZ29.
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Kumano S., Manter D., Martinez Y., Svensson R., Tatum L.I
Brown A.E., Jackson P.J.,
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                 use by non-profit institutions as long as its content is i modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
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35.5%;
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; Pred. No. 4.2;
7; Mismatches
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TS OF [LIV]-G-X(4).
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001451; Hexapep_transf.
Pfam; PF0013; hexapep; 5.
TIGRO9565; dapD; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Diaminopimelate biosynthesis; Complete proteome.
SEQUENCE 274 AA; 31184 MW; E5E923EE9584A936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METJA
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical MJ1273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q58669;
01-NOV-1997
                                                                                                                                                                                              EMBL; U67568; AAB99279.1; -.
                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
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Methanocaldococcaceae; Methanocaldococcus.
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                                                                                                                     Ptam; PF01861; DUF43; 1.
ProDom; PD011688; DUF43; 1.
Hypothetical protein; Complete
SEQUENCE 350 AA; 40420 MW;
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                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO M.JANNASCHII MJ0675 AND T.AQUATICUS HYPOTHETICAL 38.4 kDa PROTEIN IN SCSB 5'REGION (AC P25125).
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 VNWGYEESTRAWKLAPVKKKPEDIWYKSYMFRIE
                              LNWAYQQ------VQQNKEDAWIEHDVWRME 33
                                                                                                                                                              MJ1273; -.
Pro; IPR002723; DUF43.
PF01861; DUF43; 1.
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9; Conser
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                          25.8%;
llarity 26.5%;
Conservative
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                                                          Score 49.5; D
Pred. No. 18;
9; Mismatches
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2F301BF8976C22BB
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RESULT 15
SYV_CHLPN
 EMBL; AE001595
EMBL; AE002226
EMBL; AP002545
HSSP; P96142;
TIGR; CP0680;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
"Comparison of Whole genome USA.";
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
-!- CATALYTIC ACTUVITY: ATP + L-valine + tRNA(Val) = AMP + diphospi
+ L-valyl-tRNA(Val).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
Valy1-tRNA synthetase (EC 6.1.1.9)
VALS OR CPN0094 OR CP0680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae) Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYV_CHLPN
                                                                                                    InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val
Pfam; PF00133; tRNA-synt_1; 1.
PFINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequences of Chlamydia trachomatis pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
 BINDING
                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=J138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olinger L., Grimwood J., Davis R.W., Stephens R.S., "Comparative genomes of Chlamydia pneumoniae and C. Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalman S., Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99206606; PubMed=10192388;
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                                           Complete
                                                            Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                             AE002226; AAF38490.1;
AP002545; BAA98304.1;
P96142; IGAX.
                                                                                                                                                                                                                                               AE001595; AAD18247.1;
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                                                                         ; TIGR00422; vals; 1.
PS00178; AA_TRNA_LIGASE_I;
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                                           proteome
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568
567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence
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                                                         Protein biosynthesis; Ligase; ATP-binding;
"KMSKS" REGION.
ATP (BY SIMILARITY).
                              "HIGH" REGION
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RESULT 2 \$40764 hypothetical protein ZK512.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #t C;Accession: \$40764 R;Hawkins, T.; Ainscough, R. submitted to the EMBL Data Library, February 1993 A;Reference number: \$40759 A;Rocession: \$40764 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1418 <haw- 199="" 1;="" 238="" 290="" 2;="" 3;="" 529="" 557="" 588="" a;coss-references:="" a;introns:="" c;genetics:="" c;superfamily:="" caenorhabditis="" elegans="" embl:z22177;="" hypothetical="" nid:g297989;="" pid:g29="" pr<="" th=""><th>Query Match 32.6%; Score 62.5; DB 2; Lengy Best Local Similarity 25.0%; Pred. No. 1.8; Matches 12; Conservative 17; Mismatches 4; Ind. Qy 1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRME :: :::: :::: :::: :::: Db 10 RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKYK</th><th>RESULT 1 B70446 hypothetical protein aq 1687 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #tex C;Accession: B70446 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W. V. Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic ba;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70446 A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-480 AQF> A;Cross-references: GB:AE000751; NID:92984013; PIDN:AAC A;Experimental source: strain VF5 C;Genetics: A;Gene: aq_1687</th><th>30 49.5 25.8 940 2 F86502 31 49.5 25.8 1391 2 T20642 32 49.5 25.8 1397 2 E87998 34 49.5 25.8 1397 2 E87998 34 49 25.5 25.7 2 M82691 35 49 25.5 383 2 H84700 37 49 25.5 388 2 T40609 38 49 25.5 1120 2 H827032 39 49 25.5 1120 2 H827032 40 49 25.5 2925 2 T00133 41 48.5 25.3 266 2 T004751 42 48.5 25.3 339 2 T33477 44 48.5 25.3 339 2 T33477 44 48.5 25.3 3638 2 T20944 48.5 25.3 638 2 T20944 ALIGNMENTS</th></haw->	Query Match 32.6%; Score 62.5; DB 2; Lengy Best Local Similarity 25.0%; Pred. No. 1.8; Matches 12; Conservative 17; Mismatches 4; Ind. Qy 1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRME :: :::: :::: :::: :::: Db 10 RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKYK	RESULT 1 B70446 hypothetical protein aq 1687 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #tex C;Accession: B70446 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W. V. Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic ba;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70446 A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-480 AQF> A;Cross-references: GB:AE000751; NID:92984013; PIDN:AAC A;Experimental source: strain VF5 C;Genetics: A;Gene: aq_1687	30 49.5 25.8 940 2 F86502 31 49.5 25.8 1391 2 T20642 32 49.5 25.8 1397 2 E87998 34 49.5 25.8 1397 2 E87998 34 49 25.5 25.7 2 M82691 35 49 25.5 383 2 H84700 37 49 25.5 388 2 T40609 38 49 25.5 1120 2 H827032 39 49 25.5 1120 2 H827032 40 49 25.5 2925 2 T00133 41 48.5 25.3 266 2 T004751 42 48.5 25.3 339 2 T33477 44 48.5 25.3 339 2 T33477 44 48.5 25.3 3638 2 T20944 48.5 25.3 638 2 T20944 ALIGNMENTS
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R;Kunstr, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: E69631
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R;Afconso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus. A;Reference number: Z20484; MUID:99102612; PMID:9847359
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C;Accession: E69966
C;Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lamber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Galier, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, K.; Yamamoto, H.; Yamane, K.; Yamane, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69546
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hypothetical protein AF2371 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: C69546
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A;Residues: 1-502 <JUE>
A;Cross-references: EMBL:Z28337; NID:g509352; PIDN:CAA82191.1;
C;Superfamily: Microcystis aeruginosa hypothetical protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein yqkC - Bacillus subtilis
C;Spacies: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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Nature 390, 364-370, 1997
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C;Species: Microcystis aeruginosa
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
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A; Residues: 1-152 < KLE>
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Pred. No. 16;
7; Mismatches
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Pred. No. 9.
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R/Gardner, A. submitted to the EMBL Data Library, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK524.2a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change C;Accession: T19295; T19931; T27889
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A;Residues: 1-1734 <MAR>
A;Cross-references: GB:M62830
C;Superfamily: protein kinase C zinc-binding repeat homology
C;Keywords: phosphoprotein
F;615-664/Domain: protein kinase C zinc-binding repeat homology
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R;Maruyama, I.N.; Brenner, S.
Proc. Natl. Acad. Sci. U.S.A. 88, 5729-5733, 1991
A;Title: A phorbol ester/diacylglycerol-binding protein encoded by the unc-13 gene A;Reference number: A41101; MUID:91288538; PMID:2062851
A;Accession: A41101
A;Accession: A41101
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A;Molecule type: DNA
A;Residues: 1-1813 <WIL>
A;Cross-references: EMBL: Z79694; PIDN:CAB01966.1; GSPDB:GN00019; CESP:ZK524.2a
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C;Species: Caenorhabditis elegans
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Feb-1997
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A;Experimental source: strain 168
C;Genetics:
A;Gene: yqkC
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A; Residues: 1-79 < KUN>
                                       A;Residues: 1-1813 <WI2>
A;Cross-references: EMBL:Z92779; PIDN:CAB07173.1; GSPDB:GN00019; CESP:ZK524.2a
                                                                                     A; Molecule type: DNA
                                                                                                                            A; Reference number: Z19198
A; Accession: T19931
                                                                                                                                                                          submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                    A; Experimental source: clone
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Similarity 40.0%; Pred. No. 1.
8; Conservative
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Pred. No. 6.3;
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G64606
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A; Experimental source: C; Genetics:
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                                                                A; Residues: 1-90 < KUR>
                                                                                   A; Molecule type: DNA
                                                                                                                              A;Reference number: AB1807;
A;Accession: AB2102
                                                                                                                                                                                                                                                                                                                                                                              AB2102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-713 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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C;Accession: G64606

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: G64606
                                                                                                                                                                                                          R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatt DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein asr2369 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2102
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A; Residues: 1-1813 <WT3>
A; Cross-references: EMBL: Z73912; PIDN: CAA98147.1; GSPDB: GN00019; CESP: ZK524.2a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000582; GB:AE000511; NID:g2313812; PIDN:AAD07746.1; PID:g2313818 C;Superfamily: Pseudomonas D-amino acid hydantoin hydrolase (ATP-hydrolyzing) hyuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydantoin utilization protein A - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Feb-2001
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A;Cross-references: GB:BA000019; PIDN:BAB74068.1; PID:g17131461; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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8; Conservation
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; Pred. No. 76;
5; Mismatches
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Pred. No. 1.8e+02;
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Tabata, S.
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C;Species: Caer
C;Date: 15-Oct-
C;Accession: T2
R;McMurray, A
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A;Reference number: Z20330
A;Reference number: Z20330
A;Recession: T27222
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecula type: DNA
A;Residues: 1-444 «WIL»
A;Cross-references: EMBL: Z99281; PIDN:CAB16511.1; GSPDB:GN00022; CESP:Y57G11C.10
A;Experimental source: clone Y57G11C
C;Genetics:
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S75895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable L-xylulokinase (EC 2.7.1.53) - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S75895
C;Acc
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18354.1; PID:g165344 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: xylulokinase C;Keywords: phosphotransferase
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
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A; Residues: 1-495 < KAN>
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A; Introns: 332/1; 416/3
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A;Gene: CESP:Y57G11C.10
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A;Accession: S75895
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RESULT 14
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Best Local
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                                                                                                                                                      YRYKLLNWAYQQVQQNKEDA-WIEHD---VWR 31
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                                                                                             YEGNI VGQAYKELTQFYPKAGWVEHDALEIWR
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Pred.
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Pred. No. !
                                                                                                                                                                                                                                                           Score 51; DB Pred. No. 60;
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Search completed: March 26, Job time : 21.3721 secs

2003, 16:50:40

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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83360
                                                                                                                                                                                                                                                                                                                                                R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83260
                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-201 <KUR
A;Cross-references: GB:BA000019; PIDN:BAB76730.1; PID:g17134169; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein alr5031 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. (strain PCC 7120) A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AG2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PA3079 (imported) - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
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                                                                                                                                                                      A;Gene: alr5031
C;Superfamily: Synechocystis hypothetical protein slr2003
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AG2434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004732; GB:AE004091; NID:g9949186; PIDN:AAG06467.1; GSPDB:GN001:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-793 <STO>
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Best Local Similarity
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                                        9 LNWAYQQVQQNKEDAWIEHDVWRME 33
LNWQISQFQQQVGE-WLEYQSYRFE
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Pred. No.
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Pred. No. 27
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, M.; Yasuda, M.; Tabata,
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K., Lim,
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

10: /cgn2-6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

11: /cgn2-6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

12: /cgn2-6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

13: /cgn2-6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

14: /cgn2-6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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192
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length	BG	ID	Description
۲	192	100.0	34	9	US-10-011-095-20	Sequence 20, Appl
2	192	100.0	34	9	US-10-010-667A-20	•
ω	192	100.0	267	10	US-09-747-835A-50	Sequence 50, Appl
4.	192	100.0	267	10	US-09-747-835A-51	
UT	192	100.0	339	9	US-10-012-896-879	•
6	192	100.0	339	9	US-09-802-520-11	Sequence 11, Appl
7	192	100.0	339	9	US-09-895-793-879	Sequence 879, App
œ	192	100.0	339	9	US-09-895-814-879	Sequence 879, App
9	192	100.0	339	9	US-10-011-095-2	Sequence 2, Appli
10	192	100.0	339	9	US-10-010-667A-2	Sequence 2, Appli
11	192	100.0	339	10	US-09-759-143-879	Sequence 879, App
12	192	100.0	339	10	US-09-780-669-879	Sequence 879, App
13	192	100.0	339	10	US-09-822-827-879	Sequence 879, App
14	107	55.7	141	10	US-09-963-896-1	Sequence 1, Appli
15	107	55.7	173	9	US-10-011-095-8	Sequence 8, Appli
16	107	55.7	173	9	US-10-010-667A-8	Sequence 8, Appli
17	107	55.7	237	10	US-09-747-835A-15	Sequence 15, Appl
18	107	55.7	488	10	US-09-747-835A-13	Sequence 13, Appl
19	107	55.7	490	9	US-09-802-520-1	Sequence 1, Appli

RESULT 2 US-10-010-667A-20

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45	44	4.	42	41	40	39	38	37	36	ω S	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	
46.5	46.5	46.5	46.5	46.5	47	47	47	47	47	47	47.5	4.8	48	48.5	48.5	48.5	50	50	50	51	51.5	52	52	85	
24.2	24.2	24.2	24.2	24.2	24.5	24.5	24.5	24.5	24.5	24.5	24.7	25.0	25.0	25.3	25.3	25.3	26.0	26.0	26.0	26.6	26.8	27.1	27.1	44.3	
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US-09-999-832A-150	US-09-978-192A-150	US-09-978-697-150	US-09-978-295A-150	US-09-764-864-1191	US-10-007-706-1	US-10-101-464A-923	US-10-083-357-1336	US-09-739-907-79	US-09-991-258-16	US-09-739-907-171	US-09-808-880-2	US-10-101-464A-922	US-09-738-626-5483	US-09-969-528-10	US-09-764-869-974	US-09-860-670-145	US-10-040-919-2	US-09-925-300-1494	US-09-809-391-436	US-09-738-626-3647	US-09-881-752A-128	US-09-740-046-10	US-09-864-761-38670	US-10-010-667A-32	
Sequence 150, App	•	Sequence 150, App	Sequence 150, App	Sequence 1191, Ap	Sequence 1, Appli	Sequence 923, App	Sequence 1336, Ap	Sequence 79, Appl	Sequence 16, Appl	Sequence 171, App	Sequence 2, Appli	Sequence 922, App	Sequence 5483, Ap	Sequence 10, Appl	Sequence 974, App	Sequence 145, App	Sequence 2, Appli	Sequence 1494, Ap	Sequence 436, App	Sequence 3647, Ap	Sequence 128, App	Sequence 10, Appl	Sequence 38670, A	Sequence 32, Appl	

ALIGNMENTS

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RESULT 1

US-10-011-095-20

Sequence 20, Application US/10011095

Sequence 20, Application US/10011095

Publication No. US20030045682A1

GENERAL IMPORMATION:

APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)

FILE REFERENCE: 511582001610

CURRENT PILING DATE: 1990-06-01

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR FILING DATE: 1990-06-01

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1990-06-01

PRIOR FILING DATE: 1990-06-30

PRIOR PRIOR MATCHEN WOMBER: 00/091/183

PRIOR PRIOR MATCHEN WOMBER: 00/091/183

PRIOR FILING DATE: 1990-06-30

PRIOR FILING DATE: 1990-0
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APPLICANT: Zhou, Ping
APPLICANT: Wang, Dunrui
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Asundi, Vinod
APPLICANT: Dranac, Radoje T
APPLICANT: Dranac, Radoje T
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: UNMEER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NU
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APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 5.11582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
FRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PASTSEQ for Windows Version 4.0
TYPE: PRT
OPENITSM. Artificial Securics
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Best Local Similarity
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SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene
APPLICANT: Leong, Kahan
                                                                           NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50, Application US/09747835A
5. US20020146692A1
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100.0%; Pred. No. 1.1e-19;
tive 0; Mismatches 0;
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US-10-012-896-879

Sequence 879, Application US/10012896
publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hallocker, Susan L.

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Harlocker, Susan Jiang, Yuqiu Kalos, Michael D.

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APPLICANT: Ren, Felyan
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: DITMANAC, RAGOJE T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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Best Local Similarity 100.0%;
Matches 34; Conservative 0
                                                                                       Matches
                                                                                                            Query Match 100.0%; Score 192; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-18;
                                                                                                                                                                                                                                             SEQ ID NO 51
LENGTH: 267
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Patent No.
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yamazaki, Victoria
                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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                           1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 152
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5. US20020146692A1
                                                                                       34;
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Wang, Dunrui
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Liu, Chenghua
                                                                                         Conservative
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Pred. No. 1e-18;
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APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT APPLICATE 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 879
SEQ ID NO 879
LENGTH: 339
TYPE: DDT
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; Sequence 11, Application US/09802520

; Publication No. US20020187472A1
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; ORGANISM: Homo sapiens
US-10-012-896-879
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SEQ ID NO 11
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                     US-09-802-520-11
                                                                                 Query Match
Best Local 9
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                                                                  Matches
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Craig H.
TITLE OF INVENTION: STEAP-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PC-0037 US CURRENT APPLICATION NUMBER: US/09/802,520
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
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185
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Local Similarity 100.0%; Pred. No. 1.3e-18;
1es 34; Conservative 0; Mismatches 0;
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                                                                                 Local Similarity
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                  1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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                                                                Conservative
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                                                                                   100.0%; Score 192; DB 9; 100.0%; Pred. No. 1.3e-18;
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                                                                  Mismatches
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
SEQ ID NO 879
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-879
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Best Local Similarity
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APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
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 APPLICANT:
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                                                                                                           Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Vedvick, Thomas S.
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Kalos, Michael D.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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McNeill, Patricia D. Houghton, Raymond L.
                                                              Skeiky, Yasir A.W.
Hepler, William T.
                                                                                                                                                                           Retter, Marc W. Stolk, John A.
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o. US20020192763A1
                               Hural, John
                                             Henderson, Robert A.
                                                                                               Wang, Aijun
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                                                                                                                                                                                                                                          Susan L.
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FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/333,873
PRIOR APPLICATION NUMBER: 09/333,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR PRIOR PRIOR NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FABSTEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
LENGTH: 339
TYPE: PRT
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; OTHER INFORMATION: DNA
US-10-011-095-2
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                                                                                                                                                           RESULT 10
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CURRENT FILING NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FRRSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
                                                                 Sequence 2, Application US/10010667A Publication No. US20030055217A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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APPLICANT: Afar, Daniel APPLICANT: Hubert, Rene S APPLICANT: Leong, Kahan
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APPLICANT: Saffran, Douglab C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arth
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Similarity 100.0%;
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nilarity 100.0%; Pred. No. 1.3e-18;
Conservative 0; Mismatches o.
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Pred. No. 1.3e-18;
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FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Raitano, Arthur B.

APPLICANT: Safiran, Douglas C.

APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO

FILE REFERENCE: 511582001601

CURRENT APPLICATION NUMBER: US/10/010,667A

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/081,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

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PRIOR APPLICATION NUMBER: 60/091,183
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Best Local Similarity
Matches 34; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                Query Match
Best Local Similarity
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fanger, Gary R. Retter, Marc W. Stolk, John A.
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Dillon, Davin C.
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Carter, Darrick
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Kalos, Michael D.
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Pred. No. 1.3e-18;
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Pred. No. 1.3e-18;
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RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI

RESULT 12 US-09-780-669-879

sequence 879, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:

PPLICANT:

, Jiangchun llon, Davin C.

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RESULT 13
US-09-822-827-879
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-879
                                                                                                   ; ORGANISM: Homo sapiens
US-09-822-827-879
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SOFTWARE: Fab.
SEQ ID NO 879
SEQTH: 339
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CURRENT FILING DATE: 2001-03-28
NUMBER OF SEG ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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                                                                  Query Match
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                                  Matches
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
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Local Similarity 100.0%;
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1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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Hepler, William
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Carter, Darrick
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                                  Conservative
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                                                Score 192; DB 10;
Pred. No. 1.3e-18;
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Pred. No. 1.3e-18;
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US-10-011-095-8
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US-09-963-896-1
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                                                                                                                                                                                                                                   Sequence 8, Application US/10011095
Publication No. US20030045682A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
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Best Local Similarity
Matches 20; Conserv
                                                 APPLICANT:
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APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchall, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
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REGISTRATION NUMBER: 39,11:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
APPLICATION STATEMENT OF THE OPEN OPEN OF THE OPEN OF THE OPEN OPEN OF THE OPEN OPEN OPEN OPEN OPEN OF THE OPEN OPEN OPEN OPEN OPEN
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LENGTH: 141 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 218
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FILING DATE: 26-Sep-2001
CLASSIFICATION: «Unknown»
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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CLONE: 1691243
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                                                                                                                                                     Hubert, Rene
Leong, Kahan
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Corley, Neil
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Pred. No. 1.8e-07;
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CURRENT APPLICATION NUMBER: US/10/011,095;
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 173
TYPE: PRT
ORGANISM: Homo sapiens
US-10-011-095-8
Search completed: March 26, 2003, 17:04:16 Job time: 23.9302 secs
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                                                                                                                                                                                              Query Match 55.7%; Score 107; DB 9; Length 173; Best Local Similarity 58.8%; Pred. No. 2.3e-07; Matches 20; Conservative 5; Mismatches 9; Indels
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Listing first 45 summaries
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Maximum DB
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003
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US-09-134-001C-3412
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US-09-132-319-4
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Compugen Ltd.
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Sequence 3, Appli
Sequence 32, Appli
Sequence 436, App
Sequence 10, Appl
Sequence 10, Appl
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Sequence 3, Appli
Sequence 64, Appli
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RESULT 2
US-09-323-873A-2
US-09-323-873A-2
Sequence 2, Application US/09323873A
patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Athur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
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Query M Best Lo Matches	PRIOR APP PRIOR APP PRIOR FIL PRIOR FIL NUMBER OF SOFTWARE: SOFTWARE: ID NO LENGTH: TYPE: PR ORGANISM FEATURE: OTHER IN	sequence 20 Patent No. GENERAL INF APPLICANT: APPLICANT	41 42 43 44 45 RESULT 1	22666666666666666666666666666666666666
עם כו	PRIOR APPLICATION NUMBER: 60/087 PRIOR FILING DATE: 1998-06-01 PRIOR APPLICATION NUMBER: 60/091 PRIOR APPLICATION NUMBER: 60/091 PRIOR FILING DATE: 1998-06-30 NUMBER OF SEQ ID NOS: 32 SOFTWARE: FASTSEQ FOR WINDOWS VE EQ ID NO 20 LENGTH: 34 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: STEAP-1 PEPT 09-323-873A-20	20, 20, 63 WI: 63 WI: D WI: D WI: INV FINV FILL	ል ፈ ፋ ፋ ፋ ህ መ መ መ መ ህ መ መ መ መ	ቀጣል መመህ • • • • ቀጣል ቀጣል መመህ መመመጠ ቀጣል ቀጣል መመመጠ መመጠ መመጠ መመጠ መመጠ መመጠ መመጠ መመጠ መመጠ መ
tch 100.0%; Score 192 al Similarity 100.0%; Pred. No. 34; Conservative 0, Mismato RRSYRYKLLNWAYQOVQONKEDAWIEHDVWRNEI	APPLICATION NUMBER: 60/87,520 FILING DATE: 1998-06-01 APPLICATION NUMBER: 60/091,183 FILING DATE: 1998-06-30 OF SEQ ID NOS: 32 RE: FastSEQ for Windows Versic NO 20 H: 34 PRT ISM: Artificial Sequence RE: TMFORMATION: STEAP-1 PEPTIDE -873A-20	20, Application US/09323873 . 6329503 . 6329503 WFORMATION: TI: Daniel E. Afar TI: Rene S. Hubert TI: Rene S. Hubert TI: Rathur B. Raitano TI: Arthur B. Raitano TI: Arthur B. Raitano TI: Atteve Chappell Mitchell 'INVENTION: NOPEL SERPENTIN' INVENTION: EXPRESED IN ERENCE: 129.16USU2 APPLICATION UNDBER: US/09/3 FILING DATE: 1999-06-01	2222	222222222222222222222222222222222222222
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PILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
TYPE: PRI
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       Matches
                                      Query Match
Best Local
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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NAME: CERRONE, MICHAEL C
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                                                                                                                                                                                  CLONE: 1691243
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STRANDEDNESS: sir
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                                         Similarity
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Score 107; DB 3;
Pred. No. 1e-07;
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PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 173
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                                                                 ORGANISM: Homo Sapiens US-09-323-873A-32
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                                                                                                              NUMBER OF SEQ ID NOS: 32
SQPTWARE: FRAUSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 15
TYPE: PRT
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Patent No. 6329503
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Best Local Similarity
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APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129 16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                     APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
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ORGANISM: Homo Sapiens
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100.0%;
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Pred. No. 1.3e-07;
Score 85;
Pred. No.
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  DB 4; L
9.1e-06;
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Best Local Similarity

REFERENCE: 1007-05-1 REFERENCE: 1008-09-1 REFILING DATE: 1998-09-0 REFILING DATE: 1998-09-0 REFILING DATE: 1997-03-0 REFILING DATE: 1997-05-0	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 13 YQQYQQNKEDAWIEH 27
APPLICATION N FILING DATE: APPLICATION N	EARLIER APPLICATION NUMBER: 60/047,632 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,601 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/043,580 EARLIER APPLICATION NUMBER: 60/043,580 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,314 EARLIER APPLICATION NUMBER: 60/043,569 EARLIER APPLICATION NUMBER: 60/043,569 EARLIER APPLICATION NUMBER: 60/043,569 EARLIER APPLICATION NUMBER: 60/043,569 EARLIER APPLICATION NUMBER: 60/043,311 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11

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FILING DATE: 1997-05-23
                                                                                                                                                                  APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02
                                                                                                                                                                                                                                  APPLICATION NUMBER:
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11; Conservative
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NTE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: 60/047,594
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                                                                               Score 50; DB 4; Length 370;
Pred. No. 23;
6; Mismatches 10; Indels
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US-08-560-005-10; Sequence 10, Applicat; Patent No. 6001354; GENERAL INFORMATION:
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LOCATION: 1..654
OTHER INFORMATION:
US-08-560-005-10
                                                                                                                                                                                                                                                                                        US-09-418-540-10
                                                                                                                                                                                                                                              Sequence 10,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein
TITLE OF INVENTION: Acids Encoding Therefor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                         APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein.
TITLE OF INVENTION: Acids Encoding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                         CORRESPONDENCE ADDRESS:
                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               348 TYKYRGRDYAYKQKDTSEKTRVPAWCDRILWK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                 ADDRESSEE: Townsend and To
STREET: One Market Plaza,
                                                                                                                                                                                                                                                                                                                                                                                               3 SYRYKLLNWAYQQ----VQQNKEDAWIEHDVWR 31
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                 San Francisco
California
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                                                       Townsend and Townsend and Crew
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25.0%; Pred. No. 70;
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                                     Steuart Tower, Suite 2000
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COUNTRY:

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3412
LENGTH: 178
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; OTHER INFORMATION:
US-09-418-540-10
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                              S
                                                                                                                                      ; TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-134-001C-3412
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3412, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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                                                                   Best Local Similarity Matches 10; Conserv
                                                                                                    Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION UNMERS: 29,684
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: EPIDERWIDIS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 10:
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COMPUTER READAB:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
LENGTH: 654 amino acid
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APPLICATION NUMBER: US 08/560,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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RONHSKSQSDWNHQQNQQHK-DAW 161
                                RRSYRYKLLNWAYQQVQQNKEDAW 24
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                                                                     Conservative
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14-OCT-1999
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                                                                                     24.7%;
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                                                                                     Score 47.5;
Pred. No. 22;
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Pred. No. 70;
                                                                     Mismatches
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RESULT 12
US-09-332-319-4
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Best Local Similarity
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US-09-428-517-2
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US-09-121-979-4
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APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1999-02-16
                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09121979
Patent No. 6159709
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CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                     LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Recombinant OTHER INFORMATION: Oleandolide PKS
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TYPE: PRT
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                                                                                                          8 LINWAYQQVQQNKEDAWIEHDVW 30
                                                                         LANW-----KPKEDPWEQHAKW
                                                                                                                                                Conservative
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39.1%;
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Pred. No.
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Pred. No. 7.7e+02;
4; Mismatches 10;
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; Sequence 4, Application US/09332319
Patent No. 6171821
; GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin

APPLICANT: Liston, Peter

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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: XIAP IRES AND USES THEREOF FILE REFERENCE: 07891/021002

CURRENT APPLICATION NUMBER: US/09/332,319

CURRENT FILING DATE: 1999-06-14

EARLIER APPLICATION NUMBER: 09/121,979

EARLIER FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PASESEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 236

TYPE: PRT

ORGANISM: Homo Bapiens
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US-09-239-867-2
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TITLE OF INVENTION: METHODS AND COMPOUNDS FOI
TITLE OF INVENTION: METHODS AND COMPOUNDS FOI
TITLE OF INVENTION: MALE PERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
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Best Local S
Matches 9
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GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al
                                                                                                                                                                                                                                                                          Sequence 2, Application US/08746789A Patent No. 5789200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.0%;
Best Local Similarity 39.1%;
Matches 9; Conservative
            COUNTRY: USA
ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
                                                                                                                  APPLICANT: Ismail Kola, Martin J. Tymms, Ch.
TITLE OF INVENTION: A NO. 5789200el Human E.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Smithkline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
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OPERATING SYSTEM:
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WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                           Martin J. Tymms, Christine DeBouck o. 5789200el Human ETS Family Member,
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT APPLICATION NUMBER: 60/092,659
EBARLIER APPLICATION NUMBER: 60/92,659
EBARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
Search completed: March 26, Job time: 22.7442 secs
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US-09-342-648-9
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US-08-746-789A-2
                                                                                                                                                                                  US-09-342-648-9
                                                                                                                                                                                           SOPTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 885
TYPE: PRT
ORGANISM: Homo mapiens
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Best Local S
Matches 8
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                                                                                                                      Matches
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Best Local Similarity
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LENGTH: 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: No. 57892
                                                             611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: MICROSOFT WORD
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                                                                                        2 RSYRYKLINWAYQQVQQNKEDAWIEHD 28
                                                             RSSYYKSLLSAEEAAKOKKEKVWAHYE 637
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                                                                                                                        Conservative
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37.0%;
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1.1e+02;
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Maximum Match 100%
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Perfect score:
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length: 2000000000
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196.889 Million cell update
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Q9g150 sus scrofa
Q9g247 mus musculu
Q92427 mus musculu
Q92422 mus musculu
Q99412 mus musculu
Q99421 mus musculu
Q9nvb5 homo sapien
Q8tdp3 homo sapien
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Q91YU3	Q8YMT6	Q9W2E8	Q9ZLE7	Q8Z040	Q91Z87	Q8YMA3	Q9HZC9	QBUSUB	Q21449	Q8Q5X2	Q8RPU7	Q9B052	Q8YUH7	Q8W363	025402	Q8RDS2	Q9G045	Q9WF65	Q9W296	Q9FHES	Q9N7A8	09IWQ0	QSTTFO	087519	030299	Q8WWA7	Q48904	Q9RFP3
	Q8ymt6 anabaena sp	Q9w2e8 drosophila	helicoba				Q9hzc9 pseudomonas	Q8usu8 human immun	Q21449 caenorhabdi		Q8rpu7 klebsiella	7	Q8yuh7 anabaena sp	Q8w363 oryza sativ	O25402 helicobacte	N	Q9g045 mycobacteri	Q9wf65 human immun	Q9w296 drosophila	Q9fhe5 arabidopsis	Q9n7a8 leishmania	Q9iwq0 human immun	Q8ttf0 methanosarc	O87519 escherichia	O30299 archaeoglob	Q8wwa7 homo sapien		Q9rfp3 mycoplasma

ALIGNMENTS

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RESULT 1

O996U5

ID O996U5

PRELIMINARY; PRT; 264 AA.

AC Q996U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MOV-1999 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 19, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 19, Last sequence)
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBL/GenBank/DDBJ databases Sequence)
DT 01-NOV-TER 264 264
SEQUENCE FROM N.A.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases Sequence 264 AA; 31203 MM; 35C9483003557E72 CRC64;
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                                                                        Query Match
Best Local S
Matches 34
                                                                                                                                                                   Waterston R.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005061; AAD43182.1; -.

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NON TER 264 264
SEQUENCE 264 AA; 31203 MW; 35C9483003557E72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Strong C., Layman D., Graves T., Strowmatt C.;

"The sequence of Homo sapiens BAC clone CTB-87E15.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                        34;
                                                                                                    Similarity
                                                                        100.0%; ilarity 100.0%; Conservative 0;
                                                                        0;
                                                                        Score 192; DB 4;
Pred. No. 2.8e-17;
; Mismatches 0;
                                                                                                                        Length 264;
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Q95qc7 caeno Q9nq53 homo Q9yvj4 mela

homo sapien 4 melanoplus caenorhabdi

Q8te49 homo sapien Q8r554 mus musculu

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Keshi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
A Schai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Hofmann M., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Bartan M., Kohtsuki S., Langua Y., Kawaji H., Kohtsuki S.,
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Matches 34
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Q9CWR7;
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01-JUN-2001
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Mammalia; Eutheria;
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01.MAR-2001 (TrEMBLrel. 16, Last sequence update)
01.MAR-2001 (TrEMBLrel. 16, Last annotation update)
51x transmembrane endothelial antigen of PAEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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SEQUENCE 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heslan J.-M., Soulillou J.-P., Charreau B.; "Differential gene expression in endothelial cells during and LPS-mediated activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Nagasaka T., Boulday
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-EMBRYONIC STEM CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                        Hayashizaki Y.; "Function of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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tive 0;
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J.-P., Charreau
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SEQUENCE 339 AA; 39264 MW;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AY029584; AAK50537.1; -. MGD; MGI:1915678; 1010001D01Rik. SEQUENCE 339 AA; 39109 MW; 32A2C29F2E333BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic adenocarcinoma mouse prostate Cancer Res. 61:5857-5860(2001).
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Sciurognathi; Muridae;
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; Murinae; Mus
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Q924Z1;
Q1-DEC-2001
01-DEC-2001
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Q99P41;
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"A novel prostate cancer associated gene.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF335281; AAK00361.1;
EMBL; AF238865; AAL78207.1;
EMBL; AF238865; AAL78207.1;
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STRAIN-DUNNING; TISSUE-PROSTATE CANCER TUMOR;

MEDLINE=20424188; PubMed=10969787;

Steiner M.S., Zhang X., Wang Y., Lu Y.;

"Growth inhibition of prostate cancer by an adenovirus expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
        SEQUENCE FROM N.A.
Serru V., Lamblin D., Lenoir C., Manivet P.
Kellermann O., Loric S.;
"Molecular cloning and expression of mouse
Submitted (APR-2001) to the EMBL/GenBank/DD
EMBL; AY029586; AAK50539.1;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=DUNNING; TISSUE-PROSTATE CANCER
STRAIN=DUNNING; TISSUE-PROSTATE CANCER
Lu Y., Rinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel tumor suppressor gene, pressor Res. 60:4419-4425 (2000)
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                                                                                              NCBI_TaxID=10090;
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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25; Conser
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Rodentia;
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Pred. No. 3e-1
4; Mismatches
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Q9NVB5;
01-OCT-2000
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01-JUN-2002
01-JUN-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu Nakamura Y., Nagahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ10829 fis, clone NT2RP4001138 (Dudulin 2).
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                                                               Wang C., Allay J.A., Steiner M.S.;
"Second human member of pHyde family, Human pl
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL; AF262322; AAM08128.1;
                                                                                                                                                                                                                              Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AX001691; BAA91839.1; -
EMBL; AY029585; AAK50538.1; -
InterPro; IPR003006; Ig_MHC.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 488 AA; 54616 MW; BCOBCA483335AAD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Dudulin 2, a new tumor antigen expressed in Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                             SEQUENCE
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 PHYDE II.
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Vaubourdolle M., Kellermann O.,
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                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRAHRYDLVNLAVKOVLANKSHLWVEEEVWRMEI 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                              ; Metazoa;
Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                            Chordata;
Primates;
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                                               50430 MW;
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55.9%;
  50.3%;
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Last sequence up
Last annotation
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Pred. No. 3.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 4;
Pred. No. 6.5e-06;
6; Mismatches 9;
                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339886C288AEC0E2
                                               C5F7C7008D55251E CRC64;
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Loric S.;
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  96.5;
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  Length 456;
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Score

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RESULT 11
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AC 06759
AC 06759
DT 01-AI
DT 01-M
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ID QBTF0
ID QBTF0
AC QBTF0
DT 01-JU
DT 01-JU
DT 01-JU
DT Tumor
OS Homo
OC Eukar
OX NCBI
RN [1]
RN [1]
RN [1]
RN Stein
RT SEEJUS
RA SEEJUS
SQ SEQUE
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Best Local S
Matches 19
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Matches 12
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Matches 19; Conser
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067595;
01-AUG-1998
01-AUG-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TF03;
Q8TF03;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steiner M.S., Allay J.A., Wang C.;
"A novel prostate-derived tumor suppressor.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF238864; AAL78266.1; -.
                                                                                                                                                                          EMBL; AE000751; AAC07560.1; -. Hypothetical protein; Complete SEQUENCE 480 AA; 55582 MW;
                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young Graham D.B., Overbeek R., Snead M.A., Keller Feldman R.A., Short J.M., Olson G.J., Swanson "The complete genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein AQ_1687.
AQ_1687.
Aquifex aeolicus
Bacteris; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor suppressor pHyde.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                            Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                      aeolicue.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
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                                                                                                                                                                                                                                                                   complete genome icue.";
                                         RRSYR-----
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RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                  12;
                                                                                                         Similarity
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                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TYEMBLIE1. 07, Created)
(TYEMBLIE1. 07, Last sequence update)
(TYEMBLIE1. 20, Last annotation update)
protein AQ_1687.
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Primates;
                      ---YKLLNWAYQ--QVQQNKEDAWIEHDVWRME 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54402 MW; AFF16053590E6F68
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55.9%;
                                                                                                       32.6%;
25.0%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96.5; DB 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.0(
5; Mismatches
                                                                                     Pred. No. 4;
7; Mismatches
                                                                                                         Score 62.5;
Pred. No. 4;
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; Mismatches
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7BED49517A218046 CRC64;
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                                                                                                                                                                                                                                                                                      Young W.G., Lenox A.L.
ller M., Aujay M., Huben
anson R.V.;
hilic bacterium Aquifex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                ВB
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                                                                                       Indels
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ay M., Huber
                                                                                                                                480;
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RESULT: 12

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QQ QQ TEA 9 QQ AC 
RESULT
Q95QC7
ID Q99
AC Q9
DT 011
DT 01
DT 01
DT 01
CS PU
CS CA
OC EU
OX NC
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Best Local S
Matches 9
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Best Local Similarity 64.3
Matches 9; Conservative
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01-JUN-2002
01-JUN-2002
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Q8R554;
                                                                                                        Q95QC7 PRELIMINARY; PRT; 1027 AA.
Q95QC7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative TRP homologous cation channel protein (Frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57 BL/6;
Evans P.C., Coadwell W.J., Kilshaw P.J.;
Evans P.C., Coadwell murine gene, Cezanne 2."
"Isolation of a novel murine gene, Cezanne 2."
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; AJ430384; CAD23048.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Bukaryota; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
EVANS P.C., Coadwell W.J., Kilshaw P.J.;
"Isolation of a novel human gene, Cezanne 2.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ of EMBL; AJ430383; CAD23047.1;
SEQUENCE 926 AA; 100676 MW; 6E4623C2EB2C80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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CEZANNE 2.
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                                               Nematoda;
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Pred. No. 17;
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Sciurognathi; Muridae; Murinae; Mus
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                                               Chromadorea;
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Best Local Similarity 43.5%; Pred. No. 30;
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InterPro; IPR002653; Znf A20.
SMART; SM00259; Znf A20; 1.
PROSITE; PS50802; OTU; 1.
SEQUENCE 858 AA; 94401 MW; A7D6BlD280C9387F CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Q9NQ53;
Q1-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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BIOCHEMBL; AJ293573; CAB97494.1; -.
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MEDLINE=21366309; PubMed=11463333;

Evans P.C., Taylor E.R., Coadwell J., Heyninck K., Beyaert R.,
Kilshaw P.J.;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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339	339	339	339	339	339	129	129	34	34	Query Match Length DB
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ABB95387	ABG61813	AAM01282	AAM78845	AAU69927	AAY58194	AAB75315	AAB75314	AAE02787	AAY58199	ID
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Peptide #5636 enco	9	22	38	27.1	52	44
	AAM18991	22	38	27.1	52	43
bone a	AAM71318	22	38	27.1	52	42
Human brain expre	AAM58802	22	38	27.1	52	41
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Peptide #5675 enco	₽	22	38	•	52	39
human di	ABG25300	22	697	•	52.5	38
	AAY58197	21	128	29.7	57	37
Peptide 2 of human	AAE02785	22	15		85	36
ŗ	AAY58202	21	15	4	85	35
Human p-HYDE. Hom	AAB49481	22	487	0	96.5	34
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Extracellular loop	AAE02790	22	33	5	106	32
Human Six-Transmem	AAU10187	22	490	55.7	107	31
Human Tumour Suppr	ABB83366	23	488	55.7	107	30
Human protein sequ	AAB93224	22	488	55.7	107	29
	AAB85775	22	488	55.7	107	28
	AAU04564	22	488	5	107	27
Human Six-Transmem	AAU10220	22	488	5	107	26
Tumour-associated	AAU76538	23	454	55.7	107	25
Human PUMPCn prote	AAU80190	23	454	55.7	107	24
Prostate cancer-as	ABG61933	23	454	55.7	107	23
 Human six transmem 	AAE02781	22	454		107	22
Human ORF2 of Six-	AAU10188	22	454	ŗ	107	21
Human STEAP-2 prot	AAE02841	22	450	55.7	107	20
ORF3 of	AAU10189	22	419	55.7	107	19
	Q,	22	237	55.7	107	18
	AAY58195	21	173	55.7	107	17
Human prostate gro	AAY52589	21	141	55.7	107	16
Murine Tumour Supp	ABB83365	23	526	٠,	109	15
	AAB49483	22	488	56.8	109	14
$\mathbf{\sigma}$	AAM79829	22	374	ω.	179	13
	AAW86309	20	339	94.8	182	12
Human six transmem	AAE02780	22	375	100.0	192	11

ALIGNMENTS

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RESULT 1
AAY5819
ID AAY59
AAY 5419
AAY 6419
AAY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; prostate cancer; bunder antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY58199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58199 standard; peptide; 34 AA.
                                                                                                                                                                                     01-JUN-1998;
30-JUN-1998;
                                                                                                                                                                                                                                                                                                                              01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9962941-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug targetting; recombinant protein
(UROG-) UROGENESYS INC.
(AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                     98US-0087520.
98US-0091183.
                                                                                                                                                                                                                                                                                                                                   99WO-US12157.
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RESULT 2
AAE027E7
ID AAE0
XX AAE0
XX AAE0
XX AAE0
XX AAE0
XX AAE0
XX BAE0
XX B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC antigen of the prostate, ANXSB194). These peptides were used to raise CC monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype CC member of the STRAP family of proteins (AAYSB194-YSB197) which show exhibit a high degree of structural conservation, but which show CC on significant structural homology to known human proteins. The STRAP-1 CC gene has been localised to chromosome 7922. STRAP-1 is thought to be a CC type IIIa membrane protein and is expressed predominantly in prostate CC calls in normal human tissues. Structurally, STRAP-1 is a 339 amino CC increacellular N- and C-termini, suggesting that it folds in a CT georgettine manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and CC throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is CC also overexpressed in certain other cancer, including bladder, colon, CC pancreatic and ovarian cancer. The function of the STRAP proteins is not CC domains, a feature which is shared by certain on channels or CC domains, a feature which is shared by certain on channels or CC gap-junction proteins (from immunohistochemical staining). STRAP-1 and CC STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP CC specific binding agents, to produce anticancer vaccines and to generate CC specific antibodies. The antibodies may be used to identify specific antibodies. The antibodies may be used to identify and propositic respectic respectability to cancer), as therapeutic cCC inhibitors or to target therapeutic agents to their site of action. STRAP CC inhibitors or to target therapeutic agents to their site of action. STRAP CC inhibitors on the cell surface, they are easily targetted by certeins are exposed on the cell surface, they are expressed mainly CC systemically administered agents, and because they are expressed mainly CC sitemically defected on other tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                င်
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                                                                                                                              Extracellular loop #2 of human STEAP-1, suitable for cloning into
                                                                                                                                                                                             06-AUG-2001
                                                                                                                                                                                                                                                               AAE02787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                        AAE02787 standard; peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAFF/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins useful as diagnostic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEONG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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SAFFRAN D C.
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Pred. No. 3.7e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human six transmembrane epithelial CC antigen of the prostate (STEAP) protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP gene is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient. Treating comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the vector encoding single chain monoclonal antibody that comprises the cancer chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly. The present sequence is extracellular loop of STEAP-1 suitable for cloning into pfc, which is used in the invention. STEAP-1 cancer is located on chromosome 7p22.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                   Human; immunosuppressive; antiarthritic; antirheumatic; nootropic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; vindicide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection; nervous system disorder; ocular disorder; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovarian; lung; extracellular loop; serpentine transmembrane antigen.
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                                                             secreted
                                                                                                                                                                                                                                                                                                    Gene 20 human secreted protein homologous amino acid sequence
                                                                                                                                                                                                                                                                                                                                                              03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75314 standard; Protein; 129
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Pred. No. 3.7e-19;
; Mismatches 0;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to polynucleotide sequences AAF63789 - AAF63836 which encode human secreted proteins AAB75260 - AAB75287. Included in tinvention are protein sequences AAB75388 - AAB75341 which are fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-071257/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2000; 2000WO-US15135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 53-54; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200077021-A1
                       Human; immunosuppressive; antiarthritic;
antiproliferative; cytostatic; cardiant;
                                                                                                                                   03-APR-2001
                                                                                                                                                                                                                       AAB75315 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                           1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                    RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                       secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-0138632
                                                                                                                                   (first entry
                                                                                     protein sequence encoded by gene 20 SEQ ID NO:134.
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis GA;
                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 192; DB 22;
Pred. No. 1.7e-18;
; Mismatches 0;
rthritic; antirheumatic; nootropic;
cardiant; vasotropic; cerebroprotectiv
virucide; fungicide; opthalmalogical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                         rotective;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 5
AAY58194
ID AAY5
XX
AC AAY5
XX

AAY58194 standard; Protein; 339

밁 S

60

1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI

Best

Local

Similarity

100.0%; ilarity 100.0%; Conservative 0,

Score 192; DB 22; Pred. No. 1.7e-18;

Length 129;

0

Gaps

0

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of the secreted proteins and amino acid sequences with which these fragments share homology. Examples of the activities of the proteins and polynucleotides and the activities of their agonists and antagonists include, immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cyrostatic; cardiant; vasotropic; cerebroprotective; antibacterial; virucide; fungicide; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; and vulnerary activity. The protein and polynucleotide sequences, their agonists and antagonists may be useful for treating, preventing and dispossing diseases and disorders such as autoimmune diseases e.g. rheumatoid arrhitie, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, and command arrest e.g. cerebral ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection; nervous system disorder; ocular disorder; chemotaxis; food additive
                                                                                                                                                                              angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used in the identification and characterisation of the DNA and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to polynucleotide sequences AAF63789 - AAF63836 which encode human secreted proteins AAB75260 - AAB75287. Included in the invention are protein sequences AAB75288 - AAB75341 which are fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
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                                                                                                                                      of the invention.
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STRAP-1 protein.

(first entry)

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Region
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        This sequence represents a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP femily of proteins (AAY58194-Y88197) which exhibit a high degree of structural conservation, but which show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serpentine transmembrane antigen of the prostate; transmembrane domain; type IIIa membrane protein;
g
                                                                                                                                                                                                                                 01-JUN-1998;
30-JUN-1998;
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                                                                             particularly
                                                                                        Novel
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                                                                                                                                                                      (LEON/)
                                                                                                                                                                                          (AFAR/)
(HUBE/)
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                                                                                                                                                                                                               (UROG-)
significant structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             targetting; recombinant protein.
                                                                                                           2000-072832/06.
DB; AAZ49395, AJ
                                                                             proteins useful as diagnostic markers and therapeutic targets, cularly for prostatic cancer -
                                                         1; Fig 1A; 83pp; English
                                                                                                                                                            LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                         AFAR D E.
HUBERT R S.
                                                                                                                                                                                                              UROGENESYS INC.
                                                                                                                                         Hubert RS,
                                                                                                                                                                                                                                98US-0087520.
98US-0091183.
                                                                                                                                                                                                                                                                99WO-US12157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Intracellular region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                           AAZ49396.
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                                                                                                                                         Leong K,
                                                                                                                                                                                                                                                                                                                         "Intracellular region 4"
                                                                                                                                                                                                                                                                                                                                              "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                "Extracellular region 3 (AAY58200)"
                                                                                                                                                                                                                                                                                                                                                                                    "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                        "Intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                            "Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Intracellular
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 homology to
                                                                                                                                          Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                           domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                            region 2 (AAY58199)"
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 The STRAP-1
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RESULT 6
AAUG9927
IID AAUG
XX
AAUG
XX
AAUG
DT 30---
DT 30---
DT Huma
XX
Huma
XX
Huma
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Homo
OS Homo
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OS Homo
PN WO20
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PR WO21
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PR 12---
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PR 12---
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PR 10
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CC "TRAP-1 mRNA and protein expression is maintained at high levels and controllular loops. Throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is called throughout all stages of prostate cancers. Including bladder, colon, colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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                                                                                                                                       29-AUG-2000;
06-SEP-2000;
02-OCT-2000;
                                                                                                                                                                                                                                        12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene has been localised to chromosome 7p22. STRAP-1 is thought to be type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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09-MAY-2000; 2000US-0568100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001WO-US09919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Silarity 100.0%; E
Conservative 0;
                                                                                                                                2000US-0570737.
2000US-0593793.
2000US-0635783.
2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-0679426.
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                                                                                                       2000US-0685166
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Pred. No. 5.1e-18;
Mismatches 0;
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CORIXA CORP

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                            19-JUL-2000;
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                    Liu C,
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA;
                                                                                                                                          2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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                 Drmanac R
Wang J,
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J. RT, AS.J.
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Pred. No. 5.1e-18;
                    Asundi V,
ang J, Ren
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                    Zhou
F, (
                    u P,
Chen
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Carter D;
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     Cao .
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Claim

2; Page 510-512; 543pp; English

for use in vaccines

New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a

for patient

and

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AAMO128 2
AAMO1282 2
ID AAMM
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Best Local
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Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyput celectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacomodulatory activity and activity, tissue growth factor activity, hamunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; prostate-specific; diagnosis; cytostatic; gene therapy; metastasis.
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                                                                                                           WPI; 2001-425873/45.
                                                                                                                                                                                                                                      14-JAN-2000; 2000US-0483672
                                                                                                                                                                                                                                                                                                    19-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            P789P amino acid sequence.
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                                                                                                                                                                                                                                                                   16-JAN-2001; 2001WO-US01574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                       (CORI-) CORIXA CORP.
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                                                                                                                                                        Dillon DC, Mitcham JL, MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                         Meagher MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 3800-3801; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis
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Pred. No. 5.
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                                                                                                                                                         Harlocker SL, Jiang Y, Reed Retter MW, Stolk JA, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
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RESULT 9
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Best Local S
Matches 34
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08-DEC-2000; 2000US-0733748.
08-DEC-2000; 2000US-0733742.
24-JAN-2001; 2001US-263957P.
16-MAR-2001; 2001US-276791P.
16-MAR-2001; 2001US-276888P.
06-APR-2001; 2001US-281922P.
24-APR-2001; 2001US-281922P.
30-APR-2001; 2001US-286214P.
30-APR-2001; 2001US-286589P.
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                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated gears expressed in a prostate tissue
The present invention relates to methods of detecting a cancer-associated transcript in a cell from a patient. I
                                                                                                                                                                                                                                                                                                                                                                                          Gigh
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                                                                                        Claim 27; Page 312; 436pp; English
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DB; ABK92128.
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34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 192; DB 22;
Pred. No. 5.1e-18;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       Afar
                                                                                                                                                           prostate cancer-associated genes
                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                          Hevezi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
   The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 10
ABB95387
ID ABB95
XX ABB95
XX ABB95
XX ABB95
XX ABB95
XX ABB95
XX YAB95
XX YAB95
XX YAB95
XX YAB95
XX YAB95
XX Humai
XX Humai
XX Humai
XX Humai
XX Homc
XX Gene
XX Gene
XX Gene
XX Gene
XX Homc
XX Hom
XX Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  গৃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various corganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for disgnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer, as well as for identifying modulators of prostate cancer or apents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

C ABG61800-ABG61944 represent prostate cancer-associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                14-JAN-2000;
27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human P789P protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
  (MITC/)
                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1999;
12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1997;
01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002022248-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB95387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB95387 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
  XU J.
DILLON D C.
MITCHAM J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 AA;
                                                                                                                                                                   2000US-0593793.
2000US-0605783.
2000US-0636215.
2000US-0651236.
                                                                                                                                                                                                                                                                  2000US-0483672.
2000US-0536857.
2000US-0568100.
2000US-0570737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                       2000US-0657279.
2000US-0679426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0759143.
                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0020956.
98US-0030607.
98US-0115453.
98US-0159812.
98US-0232149.
99US-02388946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                         99US-0439313
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0352616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0806099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 192; DB 23;
Pred. No. 5.1e-18;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 11
AAAGO2780
ID AAAGO2780
AC AAEO2
XX
AC AAEO2
XX
DT 06-AU
DT 06-AU
DT WW Humar
XX
Humar
XX
Humar
XX
Homo
XX
FH Key
FT Regic
FT Domai
FT Domai
FT Domai
FT Regic
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                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides prostate-specific coding sequences their encoded proteins. These can be used in the diagnosis and tre of cancers, particularly prostate cancer. The present sequence is protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARL/)
(JIAN/)
(KALO/)
(KALO/)
(FANG/)
(RETT/)
(STOL/)
(DAYC/)
                                                                                                                                                                                                   Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu J, Dillon DC, Mitcham JL, Harlocke, Fanger GR, Retter MW, Stolk JA, Day CI Li SX, Wang A, Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SKEI/)
(HEPL/)
                                                                                                                                                                                                                                                                                                                        AAE02780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 879; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-255649/30.
                                  Region
                                                           Domain
                                                                                 Region
                                                                                                        Domain
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                         pancreatic
                                                                                                                                                                                                                                                  Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                                                                                                                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LISX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CART,
                                                                                                                                                                                                                                                                                                                                                                                  185 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WANG/
                                                                                                                                                                                                                                                                                                                                                                                                1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA;
                                                                                                                                                                                                                                                                        (first entry)
                                                                                         /label= Immunogenic_peptide #1
70..91
/label= Transmembrane_domain #1
                                                                                                                              Location/Qualifiers
             163.,184
                                    158..166
                                            /label= Transmembrane_domain #2
/label= Transmembrane_domain #3
                       /label= HLA-A2_binding_peptide #5
                                                                    /label= HLA-A2_binding_peptide #2
                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                         375
                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 192; DB 23;
Pred. No. 5.1e-18;
D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
epler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 12
AAW86309
ID AAW86
XX
AC AAW86
XX
DT 01-MA

AAW86309;

AAW86309 standard;

Protein; 339

₿

01-MAR-1999

(first entry)

밁 Ś

185

1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34

RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218

Query Match Best Local S Matches 34

Local Similarity

100.0%;

Score 192; DB 22; Pred. No. 5.7e-18;

Conservative

0

Mismatches

0

Indels Length

0;

Gaps

0

375;

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The present sequence is human six transmembrane epithelial antigen of CC the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell CC surface serpentine transmembrane antigens. STEAP-1 gene is located on CC chromosome 7p2.3 and is used in gene therapy. Inhibiting the development CC or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian CC and pancreatic) expressing STEAP or inhibiting growth or killing cells CC expressing STEAP in a patient, comprises administering a vaccine CC composition to the patient. Treating a patient with a cancer that CC expresses STEAP, or inhibiting growth or killing cells expressing STEAP, CC comprises administering to the patient a vector encoding single chain CC monoclonal antibody that comprises the variable domains of the heavy and CC light chains of the monoclonal antibody that specifically binds to STEAP, CC such that the vector delivers the single chain monoclonal antibody coding Sequence to the cancer cells and the encoded single chain monoclonal CC antibody is expressed intracellularly.

CC Note: The present sequence is also shown in sequence listing of the cancer cells and the single chain monoclonal end.

CC specification, but it lacks amino acid residues at its N-terminal end.
                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 1A-1B; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and t
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD07067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jakobovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000; 2000WO-US33040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-367804/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hubert RS, A;
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0455486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= HLA-A2_binding_peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Transmembrane_domain #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= HLA-A2_binding_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= HLA-A2_binding_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded by TTGTAGAAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SC,
                                                                                                                                                                                                                                                                                                                                                                                           treating
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RESULT 13
AAM79829
ID AAM79
XX
AC AAM79
XX
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                                                                                                                                                                                                                                                                                                           by expressing KIM encoding polynucleotides, to promote growth and/or by expressing KIM encoding polynucleotides. (c) promote growth and/or are upregulated in injured or regenerating (especially renal) tissues. KIM fusion proteins, conjugates, antibodies and vectors can also be used therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/ prophylaxis of conditions associated with disfunction/disregulation of KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal failure, acute nephritis). The polynucleotides can be used to produce antisense sequences which, when internalised into cells, can disrupt expression of a cellular KIM gene, also useful in therapy (e.g. to detect and quantify renal injury/disease (indicative of increased risk, or presence of, an autoimmune response or impaired function), or abnormal responses to tissue injury (indicative of increased risk, or presence of, an autoimmune response or abnormal tissue) The proteins can also be used to locate KIM-producing cells (especially specific loci, c.g. tissue growth arising from/affecting renal tissue). The proteins can arising from/affecting renal tissue), by contacting cells with an imageable KIM-binding reagent and imaging reagent accumulation.
                                                                                                                                                                                                            Query Match
Best Local S
Matches 31
                  AAM79829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 57-58; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattue ep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIM; tissue growth promotion; regeneration; racute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a kidney injury associated molecule (KIM) protein. KIM proteins can be administered therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cate RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kidney injury associated
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                                                   AAM79829 standard; Protein;
                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOJ ) BIOGEN INC.
                                                                                                                                                            1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                          RRSYRYKLLNWAYKOVOOSKEDAWVEHDVWRMEI 218
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hession CA,
                                                                                                                                                                                                                                                                                 339 AA;
                                                                                                                                                                                                                Conservative
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97US-0047490.
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                                                                                                                                                                                                                              94.8%;
91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule; kidney injury related molecule;
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Pred. No. 1.2e
3; Mismatches
                                                                                                                                                                                                                              DB 20;
L.2e-16;
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AAB49483;

AAB49483 standard; Protein; 488

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08-MAR-2001

(first entry)

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AAB49483
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19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0631561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                              (AAMBUU20) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 350; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                        inflammation.
                                                                                                                      220
                                                                                                                                                                                                                                                                               Note: Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                      reatment of cancer, leukaemia, nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                      RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                      RRSYRYKLINWAYQQVQQNKEDALIEHDVWRMEI 252
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                                                                                                                                                                      l Similarity
33; Conserv
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Wang D,
Yang Y,
                                                                                                                                                                                                                           374
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ch R;
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RESULT 15
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29-APR-1999;
26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present protein is rat p-HYDE. p-HYDE induces susceptibility of a cancer cell to cell death. The p-HYDE gene is associated with the regression of tumour growth in vivo, the induction to susceptibility to apoptosis caused by UV or chemotherapy induced DNA damage and prevention of DNA repair with the upregulation of apoptosis as the result of UV damage and the failure to repair DNA. The present sequence may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate; tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma; colorectal; pancreatic; breast; brain; gastric carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Page 20; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steiner MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000; 2000WO-US11456
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             24-DEC-2001; 2001WO-FR04188.
                                       04-JUL-2002.
                                                                WO200252274-A2
                                                                                          Mus musculus.
                                                                                                                             Neuroprotective; cytostatic; TSAP6; apoptosis; cancer; neurodegeneration; Tumour Suppressor Activated Pathway 6; TSAP6 binding protein; tumour;
                                                                                                                                                                     Murine Tumour Suppressor Activated Pathway 6, TSAP6.
                                                                                                                                                                                                02-SEP-2002
                                                                                                                                                                                                                          ABB83365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal, pancreatic, breast, brain or gastric carcinoma.
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                                                                                                                                                                                                                                                                                                                   RRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-032016/04.
)B; AAC89167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, preferably melanoma, lymphoma, leukaemia, prostate,
                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                         488 AA;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0131607.
99US-0302457.
99US-0499817.
                                                                                                                                                                                                                                                   Protein;
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Pred. No. 1.5e-06;
5; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for identifying a compound (I) that inhibits binding of TSAP (Tumour Suppressor Activated Pathway) to a TSAP6 binding protein. The present sequence is murine TSAP6, which was used in the method of the invention. (I) are useful for modulating tumour reversal and/or apoptosis for treating cancer or
                                                                                                                                                                                                                                                                                                                                         Sequence
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18-SEP-2001; 2001WO-FR02896.
                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegeneration.
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                                                1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
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1 REVIHPLATSHQQYFYKIPILV
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(c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARI

16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	N	₁	Result
47	47	47	47	47	48	48	48	48	48	48	94	94	94	108	116	Score
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565	469	431	427	233	929	488	487	456	388	172	339	339	339	338	264	Query Match Length DB
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Q04600	Q9C0F0	Q9HMR3	Q8R872	Q9SHA6	Q9QAP4	Q9NVB5	Q8TF03	Q8TDP3	Q9A0P6	Q938L7	Q924J9	Q924Z2	Q9CWR7	Q9GL50	Q9Y6U5	ID
Q04600 saccharomyc	Q9c0f0 homo sapien	Q9hmr3 halobacteri	Q8r872 thermoanaer	Q9sha6 arabidopsis	Q9qap4 cervid herp	Q9nvb5 homo sapien	Q8tf03 homo sapien	Q8tdp3 homo sapien	Q9a0p6 streptococc	Q93817 streptococc	Q924j9 mus musculu	Q924z2 mus musculu	Q9cwr7 mus musculu	Q9g150 sus scrofa	Q9y6u5 homo sapien	Description

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308	919	607	470	436	428	304	151	931	735	514	509	488	473	430	425	425	296	240	169	437	947	912	806	763	763	763	675	568
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Q9Y6U5;
Q9Y6U5;
Q1-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, I
01-DEC-2001 (TrEMBLrel. 19, I
WUGSC:H_RG087E15.1 protein (F
WUGSC:H_RG087E15.1.
                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005061; AAD43182.1; -.
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NON_TER 264 264
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MEDLINE=99063792; PubMed=9847074;

Sulston J.E., Waterston R.;

"Toward a complete human genome sequence.";

Genome Res. 8:1097-1108(1998).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Strong C., Layman D., Graves T., Strowmatt C.;

"The sequence of Homo sapiens BAC clone CTB-87E15.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                               SEQUENCE
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1 REVIHPLATSHQQYFYKIPILV
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                                                                                                                                             Similarity
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                                                                                                     100.0%; Score 116; DB 4; Length 264; ilarity 100.0%; Pred. No. 3.1e-11; Conservative 0; Mismatches 0; Indels
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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Q9CWR7;
01-JUN-2001
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Q9GL50;
01-MAR-2001
EMBL;
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TEATURECE FROM N.A.

TEATURECE FROM CELLS;
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NCBI_TaxID=9823;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria;
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STEAP OR 2410007B19RIK.
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01-DEC-2001
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                                                "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690\,(2001).
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Matches 17
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Matches 17; Conser
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01-DEC-2001
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01-DEC-2001
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Q924J9;
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319 AA; 39264 MW;
                                                                                                                     STRAIN=C57BL/6;

MEDLLNE=21371909; PubMed=11479226;

Yang D., Holt G.E., Velders M.P., Kwon B.D., Kast W.M.;

Yang D., Holt G.E., Velders M.P., Kwon B.D., Kast W.M.;

"Murine six-transmembrane epithelial antigen of the prostate, prostate-
stem cell antigen, and prostate-specific membrane antigen: prostate-
specific cell-surface antigens highly expressed in prostate cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY029584; AAK50537.1; -. MGD; MGI:1915678; 1010001D01Rik.
Transmembrane.
SEQUENCE 339
                                       EMBL; AF297098; AA
MGD; MGI:1917608;
                                                          transgenic adenocarcinoma mouse prostate
Cancer Res. 61:5857-5860(2001).
EMBL; AF297098; AAK83126.1; ~.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   STEAP
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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Rodentia;
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Sciurognathi;
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Sciurognathi; Muridae;
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    4B26A71FF559E84F CRC64;
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1.9e-07;
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                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
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Best Local S
Matches 17
                          C STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;

MEDLINB=21192684; PubMed=11296296

A Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G.,

A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin

A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin

A Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White

A Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

T "Complete genome sequence of an M1 strain of Streptococcus pyo

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

R EMBL; AE006521; AAK33638.1; -

R InterPro; IPR001991; CN4 Metransf.

R InterPro; IPR002941; N6/N4_Mtase.

R InterPro; IPR002941; N6/N4_Mtase.

R InterPro; IPR002052; N6 Mtase.

R InterPro; IPR002052; N6 Mtase.

R InterPro; IPR002052; N6 Mtase.
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Best Local Similarity
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Q9A0P6;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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Q938L7; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
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Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SPY0679.
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SEQUENCE 1
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172 AA; 1
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(Trembirel. 17, Last sequence update)
(Trembirel. 21, Last annotation update)
1 phage associated protein.
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38.1%; Pred. No. 4.
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PRINTS; PR00506; D21N6WTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
SMART; SM00470; ParBC; 1.
PROSITE; PS00092; N6 MTASE; UNKNOWN 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Proteome.
SEQUENCE 388 AA; 43690 MW; 12587B620606EBE7
                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor suppressor pHyde.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Wang C., Allay J.A., Steiner M.S.;

SEQUENCE (MAY-2000) to the EMBL/GenBank/DDBJ

EMBL; AF262322; AAM08128.1; -.

SEQUENCE 456 AA; 50430 MW; C5F7C7008D55251
                                                                                                                                                                                          SEQUENCE FROM N.A.

Steiner M.S., Allay J.A., Wang C.;

Steiner M.S., Allay J.A., Wang C.;

"A novel prostate-derived tumor suppressor.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF238864; AAL78206.1; -...

EMBL, AF238864; AAL78206.1; -...

SEQUENCE 487 AA; 54402 MW; AFF16053590E6F68 CRC64;
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Q9NVB5;
01-OCT-2000 (
01-DEC-2001 (
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Serve V., Manivet P., Lenoir C., Eschwege P., Lamblin D.,
Vaubourdolle M., Kellermann O., Loric S.;
"Dudulin 2, a new tumor antigen expressed in various human tumors.";
Submitted (Apr. 2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK001691; BAA91839.1; -.
EMBL; AY029585; AAK50538.1; -.
EMBL; AY029585; AAK50538.1; -.
InterPro; IPR003006; Ig MHC.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 488 AA; 54616 MW; BCOBCA483335AAD6 CRC64;
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alphaherpesviruses.";
Submitted (SEP-201) to the EMBL/GenBank/DDBJ
EMBL; AF078729; AAD46115.2; -.
SEQUENCE 929 AA; 100755 MW; BC0E569F92230E
                                                                                                                                                                                                                                                                                                                             "Studies of genetic relationships between bovine, and rangiferine alphaherpesviruses and improved movinus detection and identification.";
J. Clin. Microbiol. 37:1247-1253(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BANFFSHIRE 82;
MEDLINE=99221732; PubMed=10203465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein B.
cervid herpesvirus 1.
Viruses; dsDNA viruses,
Alphaherpesvirinae.
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Homo sapiens (Human)
                                                                                                                                                                                  STRAIN-BANFFSHIRE 82;
ROB C., Belak S.;
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                                                                                                                                          'Characterization of the glycoprotein B gene from ruminant
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Last sequence update)
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       BC0E569F92230BAB CRC64;
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Aoteuka S., Yoshikawa I.,
Aoteuka S., Yamamoto J., Wakamatsu
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Best Local Similarity
Matches 7; Conserv
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Best Local
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OBST872;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O-acetylhomoserine sulfhydrylase.
MET17 OR TTE2151.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter the Bacillus/Clostridium group; Clostridia;
Thermoanaerobacter the Grand Gran
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Q9SHA6;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC007661; AAD32790.1;
InterPro; IPR000345; CYCC heme bind.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
SEQUENCE 233 AA; 26250 MW; 2266F40BDICEC910 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                                                 NCBI_TaxID=119072;
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udicots; Rosidae;
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                              Q9C0P0 PRELIMINARY; PRT; 4(
Q9C0F0;
01-JUN-2001 (TrEMBLrel. 17, Created)
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01-OCT-2001 (TrEMBLrel. 18, Last annott
KIAA1713 protein (Fragment).
KIAA1713.
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Q9HMR3;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
0-acetyl homoserine.
HAL OR 'VNG2421G.
HALOBACTETIUM SP. (Strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Ya Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
Genome Res. 12:689-700(2002).
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Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003980; H3 histamine rec
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PRINTS; PR01471; HISTAMINEH3R.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                  MEDLINE=21082932; PubMed=11214970;
Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI)
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:347-355(2000).
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
[1]
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ALIGNMENTS

hypothetical protein HI0021 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: E64140
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A.; Althors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A.; Efference number: A64000; MUD:95350630; PMID:7542800
A;Reference number: A64000; MUD:95350630; PMID:7542800
A;Rocession: E64140
A;Residues: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-416 <TIGR>
A;Cross-references: GB:U32687; GB:L42023; NID:g1572955; PIDN:AAC21699.1; PID:g1572965; TJ
A;Note: best homolog was a hypothetical protein from Klebsiella pneumoniae
C;Genetics:
A;Start codon: GTG R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lie A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84273 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-177 <STO>
A;Cross-references: GB:AE004437; NID:g10580713; PIDN:AAG19555.1; GSPDB:GN00138
C;Genetics:
A;Gene: msrA
C;Superfamily: peptide methionine sulfoxide reductase peptide methionine sulfoxide reductase [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 밁 S C; Accession: G84273 Query Match Best Local (Matches Local Similarity 34 KETIRPLETGHEAYFV-LPI 1 REVIHPLATSHOOYFYKIPI Conservative 45.3%; 52 20 Score 52.5; Pred. No. 1. 4. Mismatches 1.5; BB 2 S Length 416; Indels <u>سر</u> Gaps <u>بر</u>

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g37810 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84797
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C;Keywords: chloroplast; heme; thylakoid
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A;Residues: 1-320 <REI>
A;Residues: 1-320 <REI>
A;Cross-references: EMBL:U38804; NID:g1276652; PIDN:AAC08151.1; PID:g1276731
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
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C;Species: chloroplast Porphyra purpurea
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #tex
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A;Genome: chloroplast
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A,Status: preliminary; nucleic acid sequence not shown; translation
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;Map position: 2
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Best Local (
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                                                                           105 VHPLCTQHHQHVSYVP 120
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Local Similarity 40.7%;
                                                                                                           4 IHPLATSHOOYFYKIP 19
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9; Conservative
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Pred. No. 2.1;
1; Mismatches
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Pred. No. 6
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hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YD9727.12c.
C/Species: Saccharomyces cerevisiae
C/Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C/Accession: S52682
R/Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A/Reference number: S52671
A/Rocession: S52682
A/Rocession: S52682
A/Rocession: S52682
A/Rocession: S5265 ANUR.
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                                                                                                                                           nucleoporin homolog - fission yeast (Schizosaccharomyces pombe)
C;Specises: Schizosaccharomyces pombe
C;Specises: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T39727
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21874
A;Accession: T39727
A;Accession: T39727
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA , A;Residues: 1-675 < MOS , A;Resperimental source: EMBL:AL109846; PIDN:CABS2802.1; GSPDB:GN00067; SPDB:SPBC17G9.04c A;Experimental source: strain 972h-; cosmid c17G9 C;Genetics:
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A;Gene: hal
C;Superfamily: O-succinylhomoserine (thiol)-lyase
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T39727
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A;Cross-references:
A;Map position: 4R
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A; Residues: 1-431 <STO>
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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Pred. No. 12;
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Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Paference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AI1178
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
R;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.;
Jomninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Glycine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
C;Accession: T07623
R;Hong, J.C.; Cheong, Y.H.; Naqao, R.T.; Bahk, J.D.; Cho, M.J.; Key, J.L.
Plant Physiol. 104, 793-796, 1994
A;Title: Isolation and characterization of three soybean extensin cDNAs.
A;Reference number: Z16058; MUID:94211912; PMID:8159793
A;Accession: T07623
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A;Map position: 2
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A;Residues: 1-296 <GLA>
A;Cross-references: GB:NC 003210; PIDN:CAC98911.1; PID:g16410222; GSPDB:GN00177
A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription regulator homolog lmo0833 [imported] - Listeria monocytogenes
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A; Residues: 1-169 < HON>
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N;Alternate names: hydroxyproline-rich glycoprotein HRGP2
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Best Local Similarity
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Local Similarity 57.1%;
es 8; Conservative
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                                                                                Local Similarity 41.: les 7; Conservative
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  EILHELSSTHDCAFYRI 238
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                                      EVIHPLATSHQQYFYKI 18
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                                                                                Score 46; DB Pred. No. 11; 6; Mismatches
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Pred. No.
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Pred. No. 6;
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                                                                                                                         Length 296;
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Fsihi, H.
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A; Residues: 1-425 <GLA>
A; Cross-references: GB:NC_003210; PIDN:CAC98674.1;
A; Cross-references: Strain EGD-e
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1508
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-200:
C;Accession: AD1149
                                                                          RESULT 12
T08576
                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: lin0604
C;Superfamily: O-succinylhomoserine (thiol)-lyase
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain T22F8.180 [similarity] - Arabidopsis t C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Tatches 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL592022; PIDN:CAC95836.1; PID:g16413044; GSPDB:GN00178
A;Experimental source: strain Clip11262
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A; Residues: 1-425 <GLA>
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Best Local
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Pred. No.
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Pred. No. 17;
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Dussurget, O.;
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Faihi, H.;
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probable membrane protein YPO2801 [imported] - Yersinia pestis (strain CO92) (;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0341
R;Parkhill, J; Wren, B,W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Pr
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A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132

A,Accession: C83975

A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-430 <STO>
A,Residues: 1-430 <STO>
A,Residues: 1-430 <STO>
A,Residues: BB.AP001516; GB:BA000004; NID:910175192; PIDN:BAB06322.1; GSPDB:GN00
A,Experimental source: strain C-125
A;Cross-references:
C;Genetics:
A;Gene: YPO2801
                                                                                                                                                                               A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AD0341
                                                                                                                                                                                                                                                              k;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
Nature 413, 523-527, 2001
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A;Residues: 1-428 <BEV>
A;Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.180
A;Experimental source: cultivar Columbia; BAC clone T22F8
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R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16442
A;Accession: T08576
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C;Superfamily: O-succinylhomoserine (thiol)-lyase
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A; Residues: 1-735 < KUR>
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local
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Local Similarity 63.6%;
nes 7; Conservation
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                                                              GB:AL590842; PIDN:CAC93035.1; PID:g15980773; GSPDB:GN00175
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Pred. No. 17;
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Pred. No. 17;
2; Mismatches
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RESULT 15
C70770
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70770
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Rv1327c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70776
C;Accession: C70776
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Agers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Search completed: March Job time: 14.5349 secs
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A;Gene: Rv1327c
                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-737 <COL>
A;Cross-references: GB:Z73902; GB:AL123456; NID:g3261576; PIDN:CAA98091.1; PID:e245021; F
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46.7%;
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Pred. No.
                    16:50:38
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Pred. No.
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; Gordon, S
Holroyd, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                             genome :
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 2000000000
                    A Geneseq 101002:*

//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
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116
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Copyright (c) 1993 - 2003
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapext 0.5
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	9	œ	7	6	ű	4	w	2	ь	Result No.
116	116	116	116	116	116	116	116	116	116	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
339	339	. 339	339	339	104	104	104	22	22	Query Match Length DB
23	22	22	22	21	23	22	22	22	21	B
ABG61813	AAM01282	AAM78845	AAU69927	AAY58194	ABG43832	AAM73944	ABB40417	AAE02786	AAY58198	ID
Prostate cancer-as	P789P amino acid s	Human protein SEQ	Human prostate cDN	Human STRAP-1 prot	Human peptide enco	Human bone marrow	Peptide #7923 enco	Extracellular loop	Human STRAP-1 pept	Description

4 4 5	44	43	42	41	40	9	38	37	36	35	ω 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
44.5	45	45	46	46	46	46	46	48	48	48	48	48	48	48	48	48	49	83	68	68	68	68	68	68	68	68	68	8	89	92	97	116	116	116
38.4	30.8	œ	39.7				39.7	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4			•	58.6		58.6		•	58.6			58.6	٠	76.7		83.6	ė.		100.0
1176	151	146	526	488	425	296	195	488	488	488	488	488	487	456	388	237	128	1273	576	490	454	454	454	454	454	450	419	26	339	109	95	375	374	339
22	22	22	23	22	23	23	23	23	22	22	22	22	22	22	23	22	22	22	22	22	23	23	23	22	22	22	22	22	20	20	20	22	22	23
ABB59692	ABB69782	ABG08176	ABB83365	AAB49483	ABB48993	ABB47546	ABP38703	ABB83366	AAB93224	AAB85775	AAU04564	AAU10220	AAB49481	AAB49482	ABP29233	AAU04565	AAO10072	ABG00113	ABG12306	AAU10187	AAU76538	AAU80190	ABG61933	AAE02781	AAU10188	AAE02841	AAU10189	AAE02789	AAW86309	AAY12304	AAY11840	AAE02780	AAM79829	ABB95387
Drosophila melanog	Drosophila melanog		Murine Tumour Supp	Rat p-HYDE. Rattu	Listeria monocytog	Listeria monocytog	Staphylococcus epi	Human Tumour Suppr	Human protein sequ	Human drug metabol	Human G-protein co	Human Six-Transmem	Human p-HYDE. Hom	Human p-HYDE 40.	Streptococcus poly					Human Six-Transmem	Tumour-associated	Human PUMPCn prote	ate c	Human six transmem	Human ORF2 of Six-			Extracellular loop		Human 5' EST secre	Human 5' EST secre	Human six transmem	10	Human P789P protei

ALIGNMENTS

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AAYS919

AAYS919

AAYS919

AAYS919

AAYS919

AAYS92

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                                                                                                                                                                                             01-JUN-1998;
30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY58198 standard; peptide; 22 AA.
(UROG-) UROGENESYS INC.
(AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                      01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9962941-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                             98US-0087520.
98US-0091183.
                                                                                                                                                                                                                                                                                                                                      99WO-US12157.
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ARESULT 2
AAAC02786
ID AAE0
XX AAE0
AC AAE0
XX AAE0
XX O6-A
XX Extr
XX Huma
XW Six
KW chro
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                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC member of the STRAP family of proteins (AAYSH)-1 is the protorype conshibit a high degree of structural conservation, but which show the significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22 STRAP-1 is thought to be a complete the structural human tissues. Structurally, STRAP-1 is a 339 amino cells in normal human tissues. Structurally, STRAP-1 is a 339 amino cells in characterised by six transmembrane domains and contracellular N- and C-termini, suggesting that it folds in a suppose of protein characterised by six transmembrane domains and contracellular and protein expression is maintained at high levels and contracellular and protein expression is maintained at high levels and characterised protein is contraced by certain discontraced by certain is not contracted and ovarian cancer. The function of the STRAP proteins is not command. They may be ion channels (from the presence of six transmembrane commands, a feature which is shared by certain ion channels) or composed in decident of the STRAP proteins is not composed. They may be ion channels (from the presence of six transmembrane composed in decident (from the presence of six transmembrane composed in the strap proteins in municipal station with a STRAP protein induces cellular and humoral immune responses against CSTRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP composis, and monitoring of cancers (or susceptibility to cancer), as therapeutic specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic combination/surface and prognositic response in the strapeutic disgunstic and prognositic response of STRAP expression and for therapeutic modulation/inhibition of STRAP expression and for therapeutic compositic response on the cell surface, they are easily targetted by systemically administered agents, and because they are expressed mainly compositic response on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the extracellular regions of STRAP-1 (serpentine transmembrane antigen of the prostate, AAY58194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype
six transmembrane epithelial antigen chromosome 7p22.3; cancer; prostate;
                                                                                                                                 06-AUG-2001
                                                                                                                                                                         AAE02786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAY58198-Y58200 represent synthetic peptides that correspond to the extracellular regions of STRAP-1 (serpentine transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 22; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins useful as diagnostic particularly for prostatic cancer
                                          Human; cytostatic; antiproliferative; vaccine; gene therapy;
                                                                                    Extracellular loop #1 of human STEAP-1, suitable for cloning into pFc.
                                                                                                                                                                                                               AAE02786 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           minimal side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-072832/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 116; DB 21; 100.0%; Pred. No. 7e-12; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on other tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     markers
of the prostate-1; STEAP-1; colon; bladder; pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and therapeutic targets,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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  lung;
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RESULT 3
ABB40417
ID ABB4
XX ABB4
XX ABB4
XX ABB4
XX ABB4
XX Pept
XX Pept
XX Huma
XX Homc
XX Homc
XX Homc
XX Homc
XX Homc
XX Homc
XX WO2(
XX O9-1
XX 30-1
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                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human six transmembrane epithelial CC annigen of the prostate (STEAP) protein. STEAP is a member of cell curface serpentine transmembrane antigens. STEAP gene is used in gene CC prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP (comprises administering a vaccine composition to the patient. Treating CC a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP in a patient. Treating CC a patient with a cancer that expresses STEAP, or inhibiting growth or CC killing cells expressing STEAP, comprises administering to the patient at the vector encoding single chain monoclonal antibody that comprises the CC variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the CC single chain monoclonal antibody coding sequence to the cancer cells and CC the encoded single chain monoclonal antibody is expressed contracellularly. The present sequence is extracellular loop of STEAP-1 CC suitable for cloning into pFC, which is used in the invention. STEAP-1 CC gene is located on chromosome Tp22.3.
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                           Peptide #7923 encoded by human foetal liver single exon probe
                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                          ABB40417 standard; Peptide; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 19; Page 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-367804/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jakobovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Afar DEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ovarian; extracellular loop; serpentine transmembrane antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                       1 REVIHPLATSHQQYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                          REVIHPLATSHQQYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 116; DB 2
Pred. No. 7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                           0
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30-JAN-2001; 2001WO-US00669

09-AUG-2001

WO200157277-A2

Human; foetal liver; gene expression; single exon nucleic acid probe

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RESULT 4
AAM/73 944/7
ID AAM/73 96-N
XX AAM/77
XX AAM/7
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XX Huma
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                                                                                               04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
; 2000US-0236359.
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                                                   DYNAMICS INC.
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Pred. No. 3.8e-11;
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26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234667P.
27-SEP-2000; 2000US-236559P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interestitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyspiasia; pulmonary cilary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                          measure
                                                                                                    Spatially-addressable
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                                                                        expression
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Pred. No. 3.8e-11;
; Mismatches 0;
                                                                                                                                                                                                   Rank DR;
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Claim

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 22
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from human lung comprising single exon nucleic acid probes having
12614 nucleic acid sequences mentioned in the specification, or the
complements or the 12387 open reading frames derived from the 1261
                                                                                                                                                                                                                                   Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                          Homo
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22; Conservative
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Location/Qualifiers

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This sequence represents a novel human protein, STRAP-1 (serpentine CC transmembrane antigen of the prostate). STRAP-1 is the prototype CC member of the STRAP family of proteins (AAY58194-Y58197) which comember of the STRAP family of proteins (AAY58194-Y58197) which show CC exhibit a high degree of structural conservation, but which show CC no significant structural homology to known human proteins. The STRAP-1 (see a cype IIIa membrane protein and is expressed predominantly in prostate CC cells in normal human tissues. Structurally, STRAP-1 is a 339 amino CC acid protein characterised by six transmembrane domains and CC "merpentine" manner into three extracellular and two intracellular loops. CC "serpentine" manner into three extracellular and two intracellular loops. CC "serpentine" manner into three extracellular and two intracellular and CC "TRAP-1 mRNA and protein expression is maintained at high levels and CC strap-1 mRNA and protein expression is maintained at high levels and CC also overexpressed in certain other cancers. STRAP-1 mRNA and/or protein is also overexpressed in certain other cancers, including bladder, colon, colon, colon, colon, and colon col
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DB; AAZ49395, AAZ49396.
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SAFFRAN D C.
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12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0605783.
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0657279.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0679426.
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                                                                                                                                                                                                                                                                                                                                                                                          Fanger
Li SX,
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                                                                                                                                   Claim
                                                                                                                                                                                                New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-)
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                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                                                                                                                                Page 549;
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llarity 100.0%;
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Pred. No. 1.4e-10;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Kalos MD;
Carter D;
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides antibodies raised against the polypeptides (or antigenic epitopes

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or

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RESULT 8
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Matches 22
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-CCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                                                     Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                       Claim
                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                               N-PSDB; AAK51978
                                                                                                                                                                                                                                                                                                                                                          Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                     Liu C,
Wang D,
Yang Y,
                                                                                                                                                     Page 3800-3801; 6221pp; English.
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Pred. No. 1.4e-10;
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Matches 22
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Kalos MD,
                                                                                    antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies c (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
                                                                                                                                                                                                                                                                                                                                            The present invention describes polynucleotide sequences (I) which enco prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and antibodies to (II), fusion proteins comprising (II), and isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing, monitoring for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-425873/45
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                                exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Page 510-512; 543pp; English.
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                                ent polynucleotide and amino acid sequences used of the present invention.
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100.0%; Pred. No. 1.4e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g a prostate-specific protein, treating prostate cancer in a
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24-JAN-2001; 2001US-263557P.

16-MAR-2001; 2001US-276791P.

16-MAR-2001; 2001US-276888P.

06-APR-2001; 2001US-281922P.

24-APR-2001; 2001US-286214P.

30-APR-2001; 2001US-0847046.
                     organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABG61800-ABG61944 represent prostate cancer-associated proteins.
                                                                                                                                                                                                                                                             The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue -
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08-DEC-2000; 2000US-0733288
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Pred. No. 1.4e-10;
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RESULT 11
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Best Local :
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25-FEB-1998; 98US-013667

14-JUL-1998; 98US-0115453

23-SEP-1998; 98US-0159812

15-JAN-1999; 99US-0232149

09-APR-1999; 99US-0322149

13-JUL-1999; 99US-0352616

13-VUV-1999; 99US-0439313

18-NOV-1999; 99US-0439313

18-NOV-1999; 99US-0436657

12-MAY-2000; 2000US-0436657

14-JAN-2000; 2000US-0568100

12-MAY-2000; 2000US-0568100

12-MAY-2000; 2000US-05697937

13-JUN-2000; 2000US-0505783

10-AUG-2000; 2000US-0636215

29-AUG-2000; 2000US-0657279

02-OCT-2000; 2000US-0679426

10-OCT-2000; 2000US-0679426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human P789P protein SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                     (XUJJ/)
(DILL/)
(MITC/)
(HARL/)
(JIAN/)
(KALO/)
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01-AUG-1997;
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                (LISX/)
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(VEDV/
(CART/
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       CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                   XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
JIANG M D.
KALOS M D.
FANGER G R.
RETTER M W.
                                                          STOLK J A.
DAY C H.
VEDVICK T S.
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RESULT 12
AAM79829
ID AAM79829
XX AAM79829
AC AAM79
XX O6-NO
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX O9-AU
PP 05-FE
XX 03-FE
PR 27-AP
PR 20-JU
PR 15-SE
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Best Local Similarity
Matches 22; Conserv
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27-APR-2000; 2000US-0560B75.

20-JUN-2000; 2000US-0599075.

19-JUL-2000; 2000US-0520325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell prollferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; hammlomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT, Asundi V, Zhao QA, Wang D, Wang J, Zhang J, Ren Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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DB; AAK52962.
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Pred. No. 1.4e-10;
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Wang
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Carter D;
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Claim 20; Page 350; 6221pp; English.

Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy -

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RESULT 13
AAE02780
ID AAE022
XX AAE022
AC AAE02
XX Human
DE Human
XX Human
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Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
    WO200140276-A2.
                                                                                                                                                              Domain
                                                                                                                                                                                            Domain
                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                  /label= Transmembrane_domain #1
                                                                                                                                                                                                                                                                                                                                                                                  label = Immunogenic_peptide #1
                                                                                                                                           label= Transmembrane_domain #5
                                                                                                                                                                                                                                                                                          label= Transmembrane_domain #2
                                                                                                                                                                                                                                                                                                                        label= HLA-A2_binding_peptide #2
                                                                                         label
                                                                                                                                                                                                         label= HLA-A2_binding_peptide #1
                                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                                                  label= HLA-A2_binding_peptide #5
                                                            label
                                                                                                                                                                          label= Transmembrane_domain #4
                                                                                                                  abel- HLA-A2_binding_peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                      = Transmembrane_domain #6
                               "Encoded by TTGTAGAAT"
                                                                                                                                                                                                                                 Transmembrane_domain #3
                                                         HLA-A2_binding_peptide #4
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Pred. No. 1.5e-10;
0; Mismatches 0;
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from
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the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human six transmembrane epithelial antigen of CC the prostate (STEAP): 1 protein of clone 10. STEAP is a member of cell Surface serpentine transmembrane antigens. STEAP is a member of cell CC surface serpentine transmembrane antigens. STEAP-1 gene is located on CC chromosome 7p22.3 and is used in gene therapy. Inhibiting the development CC or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian CC and pancreatic) expressing STEAP or inhibiting growth or killing cells CC expressing STEAP in a patient, comprises administering a vaccine CC composition to the patient. Treating a partient with a cancer that CC expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain CC composites administering to the patient a vector encoding single chain CC composites administering to the patient a vector encoding single chain CC composites administering to the patient a vector encoding single chain conclonal antibody that comprises the variable domains of the heavy and CC sequence to the cancer cells and the encoded single chain monoclonal contibody is expressed intracellularly.

CC sequence to the cancer cells and the encoded single chain monoclonal contibody is expressed intracellularly.

CC specification, but it lacks amino acid residues at its N-terminal end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local (
                                                                                                                                                                                                                                  Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
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N-PSDB; AAD07067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY11840 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 1A-1B; 187pp; English
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                                                                                                                                                                                                             thrombolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 116; DB 22;
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         given in AAY11716 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local :
                                                                                                                                                                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
               01-AUG-1997;
                                                                                                                                                                                                                                                                                           Human 5' EST secreted protein SEQ ID NO:335.
                                                                                                                                                                                                                                                                                                                               17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                            AAY12304 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 34; Page 577; 675pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1997;
                                              31-JUL-1998;
                                                                                                                                            Homo sapiens
                                                                                                                                                                           thrombolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVIHPLATSHQQYFYKI
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                                                                                                                                                                           anti-inflammatory; tumour inhibition.
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               97US-0905135
                                              98WO-IB01222.
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Pred. No.
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Search completed: March 26, 2003, 16:48:14 Job time : 56.7209 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                    AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12261 to AAY12514, respectively. The proteins given represent the signal peptit and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. The can also be used to develop products for diagnosis and therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 677; 824pp; English.
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  92
                           1 REVIHPLATSHQQYFYKI 18
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REVXHPLATSHOOYFYKI 109
                                                                             l Similarity
17; Conserv
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               Q9uhe8 homo sapien
P4448 h citxg pro
Q9hqg0 halobacteri
P51265 porphyra pu
Q9t034 arabidopsis
Q10638 mycobacteri
P23466 saccharomyc
Q9t034 saccharomyc
Q9t019 mus musculu
Q28920 sus scrofa
Q8th12 methanosarc
P08266 drosophila
Q8th2 methanosarc
P17471 bovine herp
P12640 bovine herp
P12640 bovine herp
P139370 escherichia
P23247 vibrio chol
Q38913 arabidopsis
Q20701 caenorhabdi
Q30130 archaeoglob
Q30745 xylella fas
Q30745 xylella fas
Q60080 vibrio mimi
P13267 bacillus su
P42346 rattus norv
P24020 sus scrofa
P02270 alligator m
Q92112 helicobacte
Q21950 caenorhabdi
P75095 mycoplasma
P26223 butyrivibri
Q85304 salmonella
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               0 sus scrofa
0 alligator m
1 helicobacte
2 helicobacte
0 caenorhabdi
5 mycoplasma
3 butyrivibri
4 salmonella
   saccharomyc
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Matches 22; Conser
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Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Philips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
15-JUN-2002 (Rel. 41, Last amnotation update)
CitxG protein [Includes: Apo-citrate lyase phosphoribosyl-dephospho-
COA transferase (EC 2.7.7.-) (Apo-ACP nucleodityltransferase); 2-(5',
triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC 4.2.-.-) (2-
(5',-triphosphoribosyl)-3'-dephospho-COA synthase)].
CITXG OR CITG OR HI0021.
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria; Proteobacteria;
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01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                          EMBL; U32687; AAC21699.1; ALT_INIT.
TIGR; HI0021; -
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                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=727;
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                                                                                                                                                                                                Transferase; Nucleotidyltransferase; Lyase; Multifunctional enzyme;
                                                                                                                                                                                                                              Pfam; PF01874; CitG;
                                                                                                                                                                                                                                                               interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION: BIFUNCTIONAL ENZYME THAT CATALYZES FORMATION OF 2-(5"-TRIPHOSPHORIBOSYL)-3"-DEPHOSPHOCENZYME-A, AND THEN THE TRANSFER OF THIS PROSTHETIC GROUP PRECURSOR TO THE APO-ACYL CARRIER PROTEIN (GAMMA CHAIN) OF THE CITRATE LYASE TO YIELD THE HOLO-ACYL CARRIER PROTEIN (BY SIMILARITY).

CATALYTIC ACTIVITY: Dephospho-CoA + ATP = 2-(5"-CATALYTIC ACTIVITY: Dephospho-CoA + adenine.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CITY FAMILY.

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CITG/MDCB
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2-(5'.-TRIPHOSPHORIBOSYL)-3'.-
DEPHOSPHOCOENZYME-A SYNTHASE.
         4467221C3DB58A96
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A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Maddocks D.G., Jablonski P.E., Krebs M., P., Angevine C.M., Dale H.,
A Maddocks D.G., Jablonski P.E., Krebs M., P., Angevine C.M., Dale H.,
A Lam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T "Genome sequence of Halobacterium species NRC-1.";
T Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
C - : FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine (By similarity).
C - : CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = C protein L-methionine S-oxide + reduced thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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15-JUN-2002
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)
methionine-S-oxide reductase) (Peptide Met(O) reductase)
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TIGRFAMs; TIGR00401; msrA; 1.
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Pfam; PF01625; PMSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005045; AAG19555.1; -. HSSP; P54149; 1FVA.
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Halobacteriaceae; Halobacterium.
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There are no restrictions
ong as its content is in
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P51265;
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Reith M.E., Munholland J.;
        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable phenylalanyl-tRNA synthetase alpha chain
(Phenylalanine--tRNA ligase alpha chain) (PheRS).
                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00190; CYTOCHROME C; 1.
Electron transport; Heme; Chloroplast; Thylakoid;
Photosynthesis; Photosystem I; Photosystem II; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002325; Apocyt F.
InterPro; IPR00345; Cyrt heme bind
Pfam; PF01333; Apocytochrome F; 1.
PRINTS; PR00610; CYTOCHROMEF.
PRINTS; PR00610; CYTOCHROMEF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Rhodo
NCBI_TaxID=2787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphyra purpurea.
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AT4G39280 OR
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                                                                                                                                                                                1 REVIHEL----ATSHQQYFYKIFILV 22
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SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN. SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (Probable). SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
                                                                                                                                                      REIIFPILSPDPAKDKQAHFFKYPIYV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics and the EMBL outstati
pean Bioinformatics Institute. There are no restrictions on
non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
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                                                                                                                                                                                                            Pred. No. 2.8
; Mismatches
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RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Ra Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Welter B., Ansorge W., Dermaler B., Mache R., Mueller M. Ra Kreis M., Delseny M., Phigdomenech P., Grival L.A., Rieger M., Bancroft I., Ra Kreis M., Delseny M., Phigdomenech P., Ratson M., Schmidtheini T., Ra Kreis M., Delseny M., Phigdomenech P., Ratson M., Schmidtheini T., Ra Kreis M., Delseny M., Phigdomenech P., Ratson M., Schmidtheini T., Robe G., Ramsperger U., Ratson M., Schwick F., Ra Bracken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Ratson M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Ramsperger U., Hilbert H., Braun M., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer E., Beradt A., Peters S., van Staveren M., De Clercq R., Ra Ra Kantonegu M., Rogers J., Cronin A., Cuail M., Bray-Allen S., Ra Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Ra Borkova D., Bloecker H., Schaffe M., Grimm M., Loehnet T.-H., Ra Borkova D., Bloecker H., Schaffe M., Grimm M., Loehnet T.-H., Ra Borkova D., Bloecker H., Schaffe M., Grimm M., Loehnet T., Ra Meumann S., Argiriou A., Vitale D., Liguori R., Pizavandi E., Ra Meumann S., Argiriou A., Vitale D., Liguori R., Pizavandi E., Ra Meumann S., Hiller R., Schmidt W., Lecharry A., Aubourg S., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Perez-Perez A., Purnelle B., Bent E., Johnson S., Tzoon D., Jesse T., Ra Kacharia P., Bevan M., Wilson R.K., de la Bastide M., Habermann N., Ra Feiber R., Bert E., Coutes M., Abu-Threideh J., Schutz K., Huang E., Spiegel L., Ra Katson J., Spiett J., Rotton B., Miller N., Greco T., Layman D., Ra Kennen J., Schutz K., Huang E., Spiegel L., Ra Katson J., Spiett J., Rotton B., Johnson A., Habert M., Johnson A., Soot K., Layman D., Ra Kennen J., Schutz M., Hoffman J., Johnson A., Shah R., Sandt
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MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:769-777(1999).

-:- CATALYTIC ACTIVITY: AIP + L-phenylalanine + tRNA(Phe)
-i- diphosphate + L-phenylalanyl-tRNA(Phe).
-:- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayer K.F.X.,
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                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (Secons end an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic (By similarity) SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SY PHE-TRNA SYNTHETASE ALPHA CHAIN SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
       AL050351; CAB43643.1;
AL161594; CAB80591.1;
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ALT_SEQ.
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                                                                                                                                                                             ute. There are no restrictions as long as its content is in removed. Usage hy
                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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_YD27_MYCTU
Q10638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Davies R., Deviln K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv1327c.
RV1327C OR MT1369 OR MTCY130.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01409; tRNA-synt 2d; 1.
TIGRPAMS; TIGR00468; pheS; 1.
PROSITE; PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SEQUENCE 474 AA; 54516 MW; OFB7F1BA07C03C77 CRC64;
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 /
                           TubercuList; Rv1327c; -.
InterPro; IPR000461; Alpha_amylase.
                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae;
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                     MT1369;
                                                                                                                       AE007010; AAK45633.1;
                                                                                                                                                Z73902; CAA98091.1;
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IPR002319; tRNA-synt_
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46.7%;
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Pred. No. 7
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                                                                                                                                                                                                                                     http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 474;
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RESULT 7
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InterPro; IPR001932; PPZC-like.
InterPro; IPR000159; RA_domain.
Pfam; PF000211; guanylate_cyc; 1.
Pfam; PF00481; PPZC; 1.
Pfam; PF00481; PPZC; 1.
Pfam; PF00560; LRR; 13.
PR.NTS; PR000000
                                                                                                                                                                  PRINTS; PRODO19; LEURICHRPT.
SMART; SM00344; CYCG; 1.
SMART; SM00370; LRR; 4.
SMART; SM00370; LRR; 74.
SMART; SM00332; LRR TYP; 3.
SMART; SM00332; PP2CC; 1.
SMART; SM00334; RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P23466;
01-NOV-1991
01-NOV-1991
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The adenylyl cyclase-encoding gene from Saccharomyces kiuyves
Gene 102:129-132(1991)
-i- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=91323718; PubMed=1864503;

Young D., O'Neill K., Broek D., Wigler M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces kluyveri (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X56042; CAA39513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
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SIMILARITY: BELONGS TO ADENYLY.
SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
SIMILARITY: CONTAINS 1 PP2C-LIKE DOMAIN.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                                                                                         Repeat;
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IPR001611; LRR.
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(Rel. 20, Last sequence update)
(Rel. 41, Last annotation update)
yclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
  632
689
680
703
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Leucine-rich
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LRR 2.
LRR 3.
LRR 4.
LRR 5.
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Pred. No.
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12;
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                                                                                                                            synthesis; Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
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T. outstation -
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RESULT 8
FRAP MOUSE
ID FRAP MOUSE
AC Q9JLN9;
DT 16-OCT-2001
            ALE CONTRACTOR OF THE PROPERTY OF THE PROPERTY
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                              Bliskovsky V., Mock B.;
"Positional cloning of mouse plasmacytoma susceptibility gene.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: ACTS AS THE TARGET FOR THE CELL-CYCLE ARREST AND
IMMUNOSUPPRESSIVE EFFECTS OF THE FKBP12-RAPAMYCIN COMPLEX.
-i- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
-i- SIMILARITY: CONTAINS 8 HEAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
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DOMAIN
                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKBP-rapamycin associated protein (FRAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                           EMBL; AF152838; AAF
HSSP; P42345; 1FAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                              [nterPro;
                                                                                                                                                                   interPro;
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                                                               j MGI:1928394; Prapl.
eerPro; IPR003151; FATC.
eerPro; IPR003151; FATC.
eerPro; IPR00357; HEAT repeat.
eerPro; IPR000403; PI3 PI4 kinase; 1.
am; PF00454; PI3 PI4 kinase; 1.
                               SM00146;
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)2260; FATC; 1.
(00146; PI3KG; 1.
(PS00915; PI3_4_KINASE_1; 1.
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Best Local S
Matches 8
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Q28920;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
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PROSITE;
PROSITE;
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REPEAT
InterPro; IPR000859; CUB_domain.
InterPro; IPR000124; Spermadhesin.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00042; CUB; 1.
PROSITE; PS00985; SPERMADHESIN_1; 1.
PROSITE; PS00986; SPERMADHESIN_2; FALSE_NEG.
PROSITE; PS01180; CUB; 1.
Heparin-binding; Glycoprotein; Fertilization; Signal.
SIGNAL 1 21 BY SIMILARITY.
CHAIN 22 137 SEMINAL PLASMA SPERM MOT
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                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: SEMINAL PLASMA OR SPERM.
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-1- SIMILARITY: BELONGS TO THE SPERMADHESIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                 EMBL; S80568; AAB35000.2; -. HSSP; P29392; 1SFP.
                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 368:420-424(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada T., Gagnon C.;
"Cloning of boar SPMI gene which is expressed spe
"esicle and codes for a sperm motility inhibitor
FEBS Lett. 368.420-424(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95361914; PubMed=7635190;
Iwamoto T., Hiroaki H., Furuichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Seminal vesicle;
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PS50290;
PS50077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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PI3_4_KINASE_3; 1.
HEAT_REPEAT; FALSE_NEG.
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SEMINAL PLASMA SPERM MOTILITY INHIBITOR.
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(See http://www.isb-sib.ch/announce/
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15-JUN-2002
15-JUN-2002
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SEQUENCE
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C2A / ATCC 35395 / DSM 2834;

STRAIN-C2A / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed=11932238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White G. W., Baulsen I.,

Perty J.G., Jarrell K.F., Jing H., Macario A.J.L., de Macario E.C.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAC
                                                                                                                                                                                                                                                                                                                                                                                                "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
Genome Res. 12:532-542(2002).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRB
                                                                                                                                         PROSITE; PS00097;
Pyrimidine biosynt
                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Pyrimidine biosynthesis; second step.
-!- SUBUNIT: Heterooligomer of catalytic and regulator
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanosarcina acetivorans.
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PYRB OR MA4502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                             2 EVIHPL-----ATSH----QOYFYKIPI 20
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 KVLHPLPRVNEIAPEVDATPHACYFEQAFYGVPI
                                                                                                                                                                          AE011170; AAM07842.1; -
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11; Conservative
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biosynthesis; Transferase; Complete proteome
308 AA; 34644 MW; 33282B438E28595C CRC64;
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41, Last annotation update)
yltransferase (EC 2.1.3.2) (
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51
36
15194
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57.9%;
                                                                          38.4*;
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B CB
                                                                            Score 44.5; D
Pred. No. 8.1;
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                                                             Pred. No. 8.1
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
                                                                                                                                                                                                                       moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                            DB 1;
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و
                                                             ω
                                                                                            Length 308;
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                                                              Gaps
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RESULT 11
RPB2_DROME
RX MEDLINE 2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeififer B.D.,
RA Harlis M.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bexendale J., Baycaktaroglu L., Beasley E.M.,
RA Benson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cayley S., Dahlke C., Ferriar C., Ferriera S.F., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paleb J.M.,
RA Melson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Zhang G., Zhang L.,
RA Globs R.A., Myers E.W., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Globs R.A., Myers E.W., Zhong W., Zhou X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POB266; Q95027; Q04155; Q9VFM7;
01-AUG-1988 (Rel. 08, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase II 140 kDa polypeptide (EC 2.7.7.6)
RNA polymerase II subunit 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPB2
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sitzler S., Oldenburg I., Peterson G., Bautz E.K.F.; "Analysis of the promoter region of the housekeeping gene DmRP140 sequence comparison of Drosophila melanogaster and Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPII140 OR CG3180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 100:155-162(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88011299; PubMed=3116266;
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Best Local Similarity
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                                                                                                                                                                                                                RFXL YEAST STANDARD; PR P46743; O1-FEB-1996 (Rel. 33, Created) 15-UUL-1998 (Rel. 36, Last seque 15-UUN-2002 (Rel. 41, Last annot Hypothetical 90.6 kDa protein ir YLR176C OR L9470.18.
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence (2000).
Science 287:2185-2195 (2000).
-!- FUNCTION: DNA-DEDENDENT RNA POLYMERASE CATALYZES THE TRANSCK-!- FUNCTION: DNA-DEDENDENT RNA POLYMERASE CATALYZES THE TRANSCK-!- FUNCTION: DNA-DEDENDENT RNA POLYMERASE CATALYZES THE TRANSCK-!- FUNCTION: Number of the polymerase catalyzes and sequence of the polymerase catalyzes.
         SEQUENCE FROM N.A.
STRAIN-5288C / AB972;
MEDLINE-97313267; PubMed-9169871;
Johnston M., Hillier L., Riles L., Albermann K., Andre B.,
Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.
Bruckner M., Goffeau A., Hebling U., Heumann K.
Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter
Louis E.J., Messenguy F., Mewes H.-W., Missga T., Mostl D.
Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E.,
                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn003276; RpI1140.
InterPro; IPR001572; RNA pol_B.
Iffam; PF00562; RNA pol_B; 1.
PROSTITE; PS01166; RNA POL_BETA; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc-finger; Metal-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X05709; CAA29180.2; --
EMBL; M62972; AAA28476.1; --
EMBL; AE03703; AAAE5024.1; --
EMBL; AE03703; A27826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content
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                                                                                                                                                        NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMER III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.

MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIFFERENT POLYPEPTIDES. SUBUNITS. THIS SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: EACH CLASS
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666 6
1176 AA;
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667
                                                                                                                                                                         Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
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Last annotation update)
protein in CBF5-DKA1 intergenic
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Pred. No. 37;
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ID -> MY (IN REF. 1).
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                                     usterhoft A.,
, Heumann K.,
e K., Kotter P.,
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RIBOSOMAL RNA
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E., Pohl T.M.,
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01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
61ycoprotein I precursor (Glycoprotein GVP-6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Portetelle D., Purnelle B., Scharfe M., Scherens B., Sch Underwood A.P., Urrestarazu Vierendeels F., Voet M., Vol
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                        InterPro; IPR000234; Glycoprot_B Pfam; PF00606; Glycoprotein_B; 1 ProDom; PD000693; Glycoprot_B; 1
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Viruses; dsDNA viruses, no RNA stage; H
Alphaherpesvirinae; Varicellovirus.
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                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        Virology 166:542-549(1988).
-!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=89020821; PubMed=2845660;
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                                                                                                      EMBL; M23257; AAA46013.1;
                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                    "Sequence of a bovine herpesvirus type-1 glycoprotein gene homologous to the herpes simplex gene for the glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31ycoprotein I precursor (Glycoprotein (Glycoprotein 16) (Glycoprotein G130).
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                                                                                                                                                                                                                                                          THE HERPESVIRUSES GLYCOPROTEIN B
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Pred. No.
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(See http://www.isb-sib.ch/announce/
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P12640;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glycoprotein I precursor (Glycoprotein GVP-6) (Glycoprotein 11A)
(Glycoprotein 16) (Glycoprotein G130) (Glycoprotein B).

GLOR UL27.
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PIR; A28877; VGBEBC.

InterPro; IPR000234; Glycoprot B.

Pfam; PF00606; Glycoprotein B; 1.

ProDom; PD000693; Glycoprot B; 1.

ProDom; PD000693; Glycoprot B; 1.
                                                                                                                                                                                                                                                                                                          MEDLINE=88300884; PubMed=2841484; Whitbeck J.C., Bello L.J., Lawrence W.C.; Whitbeck J.C., Bello L.J., Lawrence W.C.; "Comparison of the bovine herpesvirus 1 g1 gene and the herpes simplex virus type 1 gB gene."; J. Virol. 62:3319-3327(1988).

-1- SUBUNIT; DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
-1- SUBUNIT; BELONGS TO THE HERPESVIRUSES GLYCOPPOTEIN B FAMILY.
                                                                                                                                                               EMBL; M21474; AAA46055.1; -.
EMBL; Z78205; CAB01598.1; -.
EMBL; AJ004801; CAA06106.1;
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                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10323;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine herpesvirus type 1 (strain Cooper).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                             Glycoprotein;
SIGNAL
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CYTOPLASMIC (POTENTIAL)

N-LINKED (GLCNAC. .)

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GLYCOPROTEIN I.
EXTRACELLULAR.
POTENTIAL.
CYTOPLASHIC.
N-LINKED (GLCN)
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01-FEB-1995 (Rel. 31, 1
16-OCT-2001 (Rel. 40, 1
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Pfam; PF03629; DUF303; 1.
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
SIGNAL 1 21 HYPOTHETICAL PROTEIN YJHS.
CHAIN 22 326 HYPOTHETICAL PROTEIN YJHS.
CHAIN 136 AA; 36878 MW; 6E48217701678DAD CRC64;
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"Analysis of the Escherichia coli genome VI: DNA sequence region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
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MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels
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EMBL; AE000501; AAC77265.1; -.
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Pred. No.
                                                                                                                  Score 43.5;
Pred. No. 12
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                                                                                                                                             Length 326;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08 NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB		ID	Description
1	116	100.0	22	۽ و	US-10-011-095-19	Sequence 19, Appl
N	116	100.0	22	9	US-10-010-667A-19	Sequence 19, Appl
ω	116	100.0	104	10	US-09-864-761-47234	Sequence 47234, A
44	116	100.0	267	10	US-09-747-835A-50	Sequence 50, Appl
ψı	116	100.0	267	10	US-09-747-835A-51	Sequence 51, Appl
თ	116	100.0	339	ø	US-10-012-896-879	Sequence 879, App
7	116	100.0	339	9	US-09-802-520-11	Sequence 11, Appl
80	116	100.0	339	ø	US-09-895-793-879	Sequence 879, App
9	116	100.0	339	ø	US-09-895-814-879	Sequence 879, App
10	116	100.0	339	9	US-10-011-095-2	Sequence 2, Appli
11	116	100.0	339	9	US-10-010-667A-2	Sequence 2, Appli
12	116	100.0	339	10	US-09-759-143-879	Sequence 879, App
13	116	100.0	339	10	US-09-780-669-879	Sequence 879, App
14	116	100.0	339	10	US-09-822-827-879	Sequence 879, App
15	68	58.6	490	ø	US-09-802-520-1	Sequence 1, Appli
16	48	41.4	237	10	US-09-747-835A-15	Sequence 15, Appl
17	4.8	41.4	488	10	US-09-747-835A-13	Sequence 13, Appl
18	4 2	36.2	314	10	US-09-815-242-10794	Sequence 10794, A
19	42	36.2	1140	φ	US-09-950-634-4	Sequence 4, Appli

RESULT 2 US-10-010-667A-19

RESULT 1 08-10-011-095-19 ; Sequence 19, Application US/10011095 ; Publication No. US20030045682A1		45	44	43	42	41		39	38	37	3 6	3 5	34	ω ω	32	Ц	0	29	28	27	26	25	24	23	22	21	20
-095-19 19, A		39	39	39	9	<u>و</u> ن 9	<u>د</u> و	39	39	39	39	39	39	ب 9	3 9	39	39.5	40	40	40	40	40	40	40	40	41	42
9 Applica		33.6	w	w	w	33.6		w	33.6	33.6	33.6	33.6	33.6	33.6	33.6		34.1	34.5	34.5	34.5	34.5	34.5	34.5	34.5	Δ	35.3	O.
tion US		875	875	870	870	870	854	854	854	777	777	777	636	353	339	64	133	1536	437	437	437	430	359	206	59	469	2549
/10 82A		9	ø			9					ø		φ	9	12	10	10	9	10	9	9	10	9	12	9	10	9
110	ALIGNMENTS	-10-007-747-2	US-09-945-901-28	US-10-038-937-30	US-10-007-747-30	US-09-945-901-30	US-10-038-937-32	US-10-007-747-32	US-09-945-901-32	US-10-038-937-16	US-10-007-747-16	US-09-945-901-16	US-09-738-626-5590	US-10-007-343-2	US-10-067-291-1	US-09-864-761-45491	US-09-734-569-20	US-10-043-487-344	US-09-919-932-2	US-09-746-660A-2	US-09-738-626-4226	US-09-799-777-62	US-10-055-364-48	US-10-127-733-2	US-10-097-065-147	US-09-866-582-10	US-09-950-634-3
		28,	28,	30,	ω 0.	30,	ա 22 •	32,		16,	16,		55.5	٦	Sequence 1, Appli	Sequence 45491, A	Sequence 20, Appl	Sequence 344, App		Sequence 2, Appli		Sequence 62, Appl	8	Sequence 2, Appli		Sequence 10, Appl	Sequence 3, Appli

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RESULT 1
US-10-01-095-19
; Sequence 19, Application US/10011095
; Publication No. US20030045682A1
; Publication Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Mitchell, Steve Chappell
; Publication Nousean US/10/011,095
; CURRENT APPLICATION NOUSEER: US/10/011,095
; CURRENT FILING DATE: 1999-06-01
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 00/087,520
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 00/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 00/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 00/087,520
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INFORMATION

Application US/10010667A

US20030055217A1

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TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR APPLICATION PCT/US01/00666 PRIOR APPLICATI
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APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: MOVELS CAPPENT OF INVENTION MOVINGER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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Best Local Similarity
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LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47234, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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Chen, Wensheng
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2001-01-30
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100.0%; Pred. No. 7.4e-12;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. US2002014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47234
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                              APPLICANT: Zhang, Jie
APPLICANT: Ren. Felyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROT
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-01-29
                                                                                                    PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN EVALUE 5.60e+00
OTHER INFORMATION: EST HUMAN HIT: BE875216.1, EVALUE 2.00e-54
                                                               PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/552,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
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                     APPLICATION NUMBER: US
                                          FILING DATE:
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22; Conservative
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Liu, Chenghua
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Wang, Dunrui
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                     09/488,725
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Pred. No. 4.4e-11;
; Mismatches 0;
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APPLICANT: Zhou, Ping
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Zhang, Dunrui
APPLICANT: Zhang, Dunrui
APPLICANT: Zhang, Dunrui
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
ITILE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION NUMBER: US 09/747,835A
CURRENT FALING DATE: 2000-01-20-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/520,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/52,317
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-835A-50
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                                                                                                                     Sequence 879, Application No. US20 GENERAL INFORMATION:
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SEQ ID NO 51
LENCTH: 267
TYPE: PRT
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Best Local Similarity
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Patent No. US20020146692A1
APPLICANT:
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                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Liu, Chenghua
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   Harlocker, Susan L.
                                                                                                                                                         Application US/10012896
o. US20020183251A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
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US-10-012-896-879
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                                                                                                                                                                                                     TITLE OF INVENTION: STEAP-RELATED PROTEIN FILE REFERENCE: PC-0037 US CURRENT APPLICATION NUMBER: US/09/802,520 CURRENT FILING DATE: 2001-03-09 NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 339
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 2001-12-10
UNUBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
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APPLICANT: Lal, Preeti
APPLICANT: Faris, Mary
APPLICANT: Chen, Huel-Mei
APPLICANT: Ison, Craig H.
                                             Query Match
Best Local Similarity
Matches 22; Conserv
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REVIHPLATSHQQYFYKIPILV 22
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Hepler, William
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Kalos, Michael D.
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Vinals de Bassols, Carlota
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Carter, Darrick
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Thomas
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CURRENT APPLICATION NUMBER: US/09/895,793; CURRENT FILING DATE: 2001-06-29; NUMBER OF SEQ ID NOS: 982; SOFTWARE: FRSEQ FOR WINDOWS Version 3.0 SEQ ID NO 879 LENGTH: 339; TYPE: PRT ORGANISM: Homo sapiens
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publication No. US200201927
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
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Publication No.
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
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Mitcham, Jennifer L.
Hural, John
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Vedvick, Thomas
Carter, Darrick
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                              Skeiky, Yasir A.W.
Hepler, William T.
                                                                Wang, Aijun
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Kalos, Michael D.
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Vinals de Bassols, Carlota
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Carter, Darrick
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Kalos, Michael D.
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                                                                               Li, Samuel X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                              Craig H.
ick, Thomas S
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                 Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 116; DB 9;
100.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 339;
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CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/23,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: DNA
US-10-011-095-2
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APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
FILE REFERENCE: 511582001610
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10011095 Publication No. US20030045682A1
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                                                                                                                               Matches
                                                                                                                                             Query Match
Best Local Similarity
Matches 22: Conserv
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APPLICANT:
APPLICANT:
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ORGANISM: Artificial Sequence
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                                    1 REVIHPLATSHOOYFYKIPILV 22
REVIHPLATSHOOYFYKIPILV 113
                                                                                                                               22;
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                                                                                                                               Conservative
                                                                                                                                                          100.0%;
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                                                                                                                                                             Score 116; DB 9;
Pred. No. 1.7e-10;
                                                                                                                               Mismatches
                                                                                                                                                                                       Length 339;
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Sequence 2, Application US/10010667A Publication No. US20030055217A1 GENERAL INFORMATION:

APPLICANT: Afar, Daniel

RESULT 11 US-10-010-667A-2

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FRSCEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-143-879
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PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 2
                 Query Match
Best Local Similarity
Watches 22; Conserve
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US-09-759-143-879
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APPLICANT: Xu, Jia
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CURRENT FILING DATE: 2001-12-06
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APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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es 22; Conservative
1 REVIHPLATSHQQYFYKIPILV 22
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US20020022248A1
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Ang, Kahan
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fanger, Gary R. Retter, Marc W. Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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                                100.0%; Score 116; DB 10; 100.0%; Pred. No. 1.7e-10; vrive 0; Mismatches 0;
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Pred. No. 1.7e-10;
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APPLICANT: Houghton, Raymond L.
TITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-780-669-879
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                                                             ; TYPE: PRT; ORGANISM: Homo sapiens US-09-822-827-879
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                                                                                                    GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: DET
                                                                                                                                                                                                                                                                                Sequence 879, Application US/09822827 Patent No. US20020081680A1
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Best Local Similarity
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Query Match
Best Local Similarity
Matches 22; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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Hepler, William
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Carter, Darrick
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100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 116; DB 10; 100.0%; Pred. No. 1.7e-10;
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Score 116; DB 10;
Pred. No. 1.7e-10;
Mismatches 0;
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                              Length 339;
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   Indels
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   Gaps
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RESULT 15
US-09-802-520-1
US-09-802-520-1
Sequence 1, Application US/09802520
Publication No. US20020187472A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Faris, Mary
APPLICANT: Gen, Huei-Mei
APPLICANT: Gen, Craig H.
ITILE OF INVENTION: STEAP-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL PROGRAM
SEQ ID NO 1
LENGTH: 490
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020187472A1 7492448CD1
US-09-802-520-1
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Search completed: March 26, 2003, 17:04:15 Job time: 15.8372 secs
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                                                                                                                                                     Query Match 58.6%; Score 68; DB 9; Length 490; Best Local Similarity 65.0%; Pred. No. 0.0083; Matches 13; Conservative 2; Mismatches 5; Indels
                                                                           1 REVIHPLATSHQQYFYKIPI 20
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233 RDVIHPYARNQQSDFYKIPI 252
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Database
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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80
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seq length:
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    Issued Patents AA.*

1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/backfIles1.pep:*
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                           Length
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     GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
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 US-09-323-873A-19
US-09-323-873A-2
US-09-134-001C-3548
US-08-682-847-2
US-09-357-251-24
US-09-357-251-24
US-09-012-515A-12
US-09-012-515A-12
US-09-012-504A-12
US-09-012-504A-12
US-08-471-112A-3
PCT-US95-06722-12
US-08-581-148C-18
US-08-581-148C-18
US-08-581-148C-18
US-08-581-148C-18
US-08-66-490-2
US-08-66-490-2
US-08-282-197C-60
US-08-282-197C-60
US-08-282-1912-60
US-08-282-1913-18-3
US-08-282-1913-18-3
US-08-413-118-3
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US-08-720-229-21	US-08-473-446-7	US-08-804-439A-21	US-08-413-118-7	US-08-220-151-7	US-08-185-432-4	US-08-185-432-2	US-09-411-628-4	US-09-291-023A-15	US-09-291-023A-14	US-09-291-023A-4	US-09-291-023A-2	US-09-461-474-4	US-08-185-432-5	US-09-219-797-2	US-07-903-029-6	US-09-134-001C-2858	US-08-4/3-446-106
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
21, App]	7, Appli	21, Appl	7, Appl:	7, Appl:	4, Appl:	2, Appl	4, Appl	15, App	14, App	4, Appl	2, Appl	4, Appl	5, Appl	2, Appl	6, Appl	æ	ddw 'enr

ALIGNMENTS

RESULT 1 US-09-323-873A-19

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Sequence 19, Application US/09323873A

PRICENT NO. 622903

GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Aphlicant: Rene S. Rubert
APPLICANT: Rene S. Rubert
APPLICANT: Achian Leong
APPLICANT: Achian Leong
APPLICANT: Achian Leong
INTILE OF INVENTION: EXPERSED IN THE TRANSMEMBRANE ANTIGENS
ITITLE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: EXPERSED IN HUMAN CANCERS AND USES THEREOF
ITILE OF INVENTION: MOMBER: 60/09/323,873A
CURRENT APPLICATION NUMBER: 60/09/323,873A
CURRENT FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/09/323,873A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/09/323,873A
CURRENT APPLICATION NUMBER: 60/09/323,873A
CURRENT PRI
PRIOR APPLICATION NUMBER: 60/09/323,873A
CURRENT PRI
PRI
PRIOR APPLICATE AND THE 1998-06-30

PRIOR APPLICANT: Conservative 0; Mismatches 0; Indels 0; Gaps
OTHER INFORMATION: STEAP-1 PEPTIDE
US-09-323-873A-19

QUERY Match
Best Local Similarity 100.0%; Score 116; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
DB 1 REVIHPLATSHOQYFYKIPILV 22

US-09-323-873A-2
US-09
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PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-323-873A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3548
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLIC
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SEQ ID NO 3548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08682847 Patent No. 5858989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.7%;
Best Local Similarity 44.4%;
Matches 8; Conservative
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: V
APPLICANT: Z
APPLICANT: E
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                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                       TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 RSLLSPLKTSYQEWQYQI 145
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FITZPATRICK, DAVID
                                    755 PAGE MILL ROAD
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VAN DEN HURK, SYLVIA
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Pred. No.
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APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Schwaber, James S.
APPLICANT: Schwaber, James S.
FITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER FILING DATE: 1999-07-20
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 284
TYPE: PRT
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                                                                                                                                US-09-357-251-24
                                       Query Match
Best Local Similarity 46...
""" hes 7; Conservative
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09357251
Patent No. 6271441
GENERAL INFORMATION:
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Best Local
                                                                                                                                               ORGANISM: Triticum aestivum
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 12-JUL-1996
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 RELVEPCTANHKRYF 674
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les 6; Conserv
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                             5 HPLATSHOOYFYKIP 19
HPARDSHOTFFLKAP 69
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                                                                            Score 42;
Pred. No.
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                                                             Mismatches
                                                                                               DB 4;
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                                                                                             Length 284;
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RESULT 6 US-09-134-001C-3888

Sequence 3888, Application US/09134001C Patent No. 6380370

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US-08-471-112A-4
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LENGTH: 319
TYPE: PRT
                                                                                                         COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,112A
FILING DATE: 06-UN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-PEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-PEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/312,023
FILING DATE: 26-SEP-1995
PRIOR APPLICATION NUMBER: US 08/312,023
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
AME: Siekman, Michael T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08471112A Patent No. 6313264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Lynn Doucette-Stamm et al ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                  REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142.0058-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEB: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
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Local Similarity 47.1%;
les 8; Conservative
                                                                                     NAME: Siekman, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
TELEPHONE: 202-408-40
TELEPAX: 202-408-4400
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Nakanishi, Koji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molnar-Kimber, Katherine L. Failli, Amedeo F.
                   202-408-4000
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Pred. No.
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Best Local Similarity
Thes 8; Conserve
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Best Local Similarity
Thes 8; Conserva
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                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-012-515A-12
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Patent No. 6
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                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08,
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:

TOPOLOGY:

177

177

177
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LENGTH: 1809 amino acids
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
943 RQLDHPLPTVHPQVTY 958
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                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: AP
                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                        1 REVIHPLATSHOOYFY 16
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One Post Office Square
                                                                                                                                                                                                       617-832-1000
617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiu, Maria Isabel
Cottarel, Guillaume
Damagnez, Veronique
VENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
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                                                    Conservative
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                                                                  36.2%;
50.0%;
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Pred. No.
                                                    2
                                                                 Score 42;
Pred. No. 3
                                                     Mismatches
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1.8e+02;
                                                                  DB 3;
3.1e+02;
                                                                              Length 1809;
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RESULT 9 US-08-360-144A-12

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APPLICANT: Berlin, V.
APPLICANT: Chiu, I.
APPLICANT: Cottarel, G.
APPLICANT: Cottarel, G.
APPLICANT: Damagnez, V.
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
FILE REFERENCE: APBI-P05-036
FILE REFERENCE: APBI-P05-036
CURRENT APPLICATION NUMBER: US/09/012,504A
CURRENT FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 08/350,144
PRIOR APPLICATION NUMBER: 08/50,795
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US-09-012-504A-12
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                                                                                    SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09012504A Patent No. 6464974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/360,144A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·09-012-504A-12
                                                                                                            SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                 NUMBER OF SEQ ID NOS:
                     ORGANISM: Mammalian
                                                               ENGTH: 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: APTELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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Local Similarity 50.0%;
les 8; Conservative
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Pred. No. 3.1e+02;
2; Mismatches 6
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Best Local Similarity 50.
                                                                      Query Match
Best Local :
                                                                                                                                                                                         TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2549 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
1683 RQLDHPLPTVHPQVTY 1698
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 26-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                   TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, YE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        943 RQLDHPLPTVHPQVTY 958
                                                                       Local Similarity
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVIHPLATSHOOVEY 16
                          1 REVIHPLATSHOOYFY 16
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                                                                                                                                                                                                                                                                                                                Siekman, Michael
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                                                           Conservative
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                                                                                                                                                  linear
                                                                                                                               peptide
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                                                                                                                                                            single
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50.0%;
                                                                       36.2%;
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                                                                       Pred. No.
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Pred. No.
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                                                           Mismatches
                                                                         4.5e+02;
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3.1e+02;
                                                                                        DB 4;
                                                                                     Length 2549;
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US-08-581-148C-18
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P. COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06722

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18,
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TITLE OF INVENTION: Immunosur
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
                           ZIP: 606016780

ZIP: 606016780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/:
FILING DATE: 20-DEC-1994
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2549 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 12, Applicat GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 08/250,795
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xia, Yiji
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2549 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 50.
                                                                                                                                                                                                                                                                                CITY: Chicago
                                                                                                                                                                                                                                           COUNTRY:
            NAME: Larcher, Carol REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 REVIHPLATSHOOYFY 16
REFERENCE/DOCKET NUMBER: 71380
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                                                                                                                                                                                                                                                S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hansen, Joel D
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nikolau, Basil J.
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Pred. No.
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                                                                                                                                      Version #1.30
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US-08-759-436-3
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                             Ś
                                                                                                                              TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-759-436-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3,
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                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                TELEFAX: 212-246-8959
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                        COMPUTE: IBM PC COMPATIBLE
COMPUTE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,436
FILING DATE: 5-Dec-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cord, Janet I.
REGISTRATION NUMBER: 33,778
REGISTRATION NUMBER: 33,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: U0
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 VIHPFA-EHIAYFILFAIPLL 193
174 VIHPFA-EHIAYFILFAIPLL 193
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Local Similarity 52.4%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                 TELEPHONE: 212-708-1935
TELEFAX: 212-246-8959
                               3 VIHPLATSHOOYF--YKIPIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                              Conservative
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                                                                               35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fatty aldehyde decarbonylase activity, recombinant molecules comprising said fragment and a method fo obtaining transformed bacterial cells and plants
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                                                                                 Score 41.5;
Pred. No. 1
                                                                   Mismatches
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RESULT 15 US-08-759-436-5

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FILING DATE: 5-Dec-1996
ATTORNEY/AGENT INFORMATION:
NAME: COZG, Janet I.
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U011063-5 **
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-708-1935
TELEPHONE: 212-246-8959
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acids
                                                                                                                                                                      US-08-759-436-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08759436 Patent No. 6437218
                                                                              Query Match
Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: Protein
NAME/KEY: Protein
LOCATION: 1.625
PUBLICATION: 1.625
PUBLICATION INFORMATION:
AUTHORS: Keijzer, Christian J.
AUTHORS: Keijzer, Christian J.
AUTHORS: Stickema, Willem J.
AUTHORS: Pereira, Andy
TITLE: Molecular characterization of the CER1 gene
TITLE: of Arabidopsis involved in epicuticular wax
TITLE: biosynthesis and pollen fertility
JOURNAL: Plant Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
STRAIN: Columbia ecotype
DEVELOPMENTAL STAGE: light and dark grown seedlings;
DEVELOPMENTAL STAGE: rosette and whole plants
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
174 VIHPFA-EHIAYFILFAIPLL 193
                                                                                                                                                                                      PAGES: 2115-2127
DATE: december-1995
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 26 West 61st Street
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                             JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY:
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                           3 VIHPLATSHQQYF--YKIPIL 21
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                                                                              35.8%; Score 41.5; DB 4; ilarity 52.4%; Pred. No. 1.1e+02; Conservative 2; Mismatches 5
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Search completed: March 26, 2003, 16:51:39 Job time: 16.0698 secs